Method for distinguishing AML subtype inv(3)(q21q26)/t(3;3)(q21q26) from other AML subtypes

The present invention is directed to a method for distinguishing AML subtype inv(3)(q21q26)/t(3;3)(q21q26) (abbreviated: AML_inv(3)) from other AML subtypes, in particular from t(8;21), t(15;17), inv(16), t(11q23)/MLL (abbreviated: AML_11q23), AML_normal (normal karyotype) and/or AML_CA (complex aberrant karyotype) by determining the expression level of selected marker genes.

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Leukemias are classified into four different groups or types: acute myeloid (AML), acute lymphatic (ALL), chronic myeloid (CML) and chronic lymphatic leukemia (CLL). Within these groups, several subcategories can be identified further using a panel of standard techniques as described below. These different subcategories in leukemias are associated with varying clinical outcome and therefore are the basis for different treatment strategies. The importance of highly specific classification may be illustrated in detail further for the AML as a very heterogeneous group of diseases. Effort is aimed at identifying biological entities and to distinguish and classify subgroups of AML which are associated with a favorable, intermediate or unfavorable prognosis, respectively. In 1976, the FAB classification was proposed by the French-American-British co-operative group which was based on cytomorphology and cytochemistry in order to separate AML subgroups according to the morphological appearance of blasts in the blood and bone marrow. In addition, it was recognized that genetic abnormalities occurring in the leukemic blast had a major impact on the morphological picture and even more on the prognosis. So far, the karyotype of the leukemic blasts is the most important independent prognostic factor regarding response to therapy as well as survival.

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Usually, a combination of methods is necessary to obtain the most important information in leukemia diagnostics: Analysis of the morphology and cytochemistry of bone marrow blasts and peripheral blood cells is necessary to establish the diagnosis. In some cases the addition of immunophenotyping is mandatory to separate very undifferentiated AML from acute lymphoblastic leukemia and CLL. Leukemia subtypes investigated can be diagnosed by cytomorphology alone, only if an expert reviews the smears. However, a genetic analysis based on chromosome analysis, fluorescence in situ hybridization or RT-

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PCR and immunophenotyping is required in order to assign all cases into the right category. The aim of these techniques besides diagnosis is mainly to determine the prognosis of the leukemia. A major disadvantage of these methods, however, is that viable cells are necessary as the cells for genetic analysis have to divide in vitro in order to obtain metaphases for the analysis. Another problem is the long time of 72 hours from receipt of the material in the laboratory to obtain the result. Furthermore, great experience in preparation of chromosomes and even more in analyzing the karyotypes is required to obtain the correct result in at least 90% of cases. Using these techniques in combination, hematological malignancies in a first approach are separated into chronic myeloid leukemia (CML), chronic lymphatic (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within the latter three disease entities several prognostically relevant subtypes have been established. As a second approach this further sub-classification is based mainly on genetic abnormalities of the leukemic blasts and clearly is associated with different prognoses.

The sub-classification of leukemias becomes increasingly important to guide therapy. The development of new, specific drugs and treatment approaches requires the identification of specific subtypes that may benefit from a distinct therapeutic protocol and, thus, can improve outcome of distinct subsets of leukemia. For example, the new therapeutic drug (STI571, Imatinib) inhibits the CML specific chimeric tyrosine kinase BCR-ABL generated from the genetic defect observed in CML, the BCR-ABL-rearrangement due to the translocation between chromosomes 9 and 22 (t(9;22) (q34; q11)). In patients treated with this new drug, the therapy response is dramatically higher as compared to all other drugs that had been used so far. Another example is the subtype of acute myeloid leukemia AML M3 and its variant M3v both with karyotype t[15;17)(q22; q11-12). The introduction of a new drug (all-trans retinoic acid - ATRA) has improved the outcome in this subgroup of patient from about 50% to 85 % long-term survivors. As it is mandatory for these patients suffering from these specific leukemia subtypes to be identified as fast as possible so that the best therapy can be applied, diagnostics today must accomplish sub-classification with maximal precision. Not only for these subtypes but also for several other leukemia subtypes different treatment approaches could improve outcome. Therefore, rapid and precise identification of distinct leukemia subtypes is the future goal for diagnostics.

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Thus, the technical problem underlying the present invention was to provide means for leukemia diagnostics which overcome at least some of the disadvantages of the prior art diagnostic methods, in particular encompassing the time-consuming and unreliable combination of different methods and which provides a rapid assay to
5   unambiguously distinguish one AML subtype from another, e.g. by genetic analysis.

According to Golub et al. (Science, 1999, 286, 531-7), gene expression profiles can be used for class prediction and discriminating AML from ALL samples. However,
10   for the analysis of acute leukemias the selection of the two different subgroups was performed using exclusively morphologic-phenotypical criteria. This was only descriptive and does not provide deeper insights into the pathogenesis or the underlying biology of the leukemia. The approach reproduces only very basic knowledge of cytomorphology and intends to differentiate classes. The data is not
15   sufficient to predict prognostically relevant cytogenetic aberrations.

Furthermore, the international application WO-A 03/039443 discloses marker genes the expression levels of which are characteristic for certain leukemia, e.g. AML subtypes and additionally discloses methods for differentiating between the
20   subtype of AML cells by determining the expression profile of the disclosed marker genes. However, WO-A 03/039443 does not provide guidance which set of distinct genes discriminate between two subtypes and, as such, can be routineously taken in order to distinguish one AML subtype from another.

25   The problem is solved by the present invention, which provides a method for distinguishing AML subtype AML_inv(3) from other AML subtypes in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, and/or 4,

30   wherein

        a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a negative fc value, and/or

        a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a positive fc value,

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is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from all other subtypes ,

and/or wherein

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a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from all other subtypes ,

10   and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a positive fc value,

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is indicative for the presence of AML_inv(3) when AML_inv(3) is distinguished from all other subtypes ,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a negative fc value, and/or

20

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a positive fc value,

is indicative for the presence of AML_normal when AML_normal is distinguished from all other subtypes ,

and/or wherein

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a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a positive fc value,

is indicative for the presence of AML_t(15;17) when AML_t(15;17) is distinguished from all other subtypes ,

30

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a positive fc value,

is indicative for the presence of AML_t(8;21) when AML_t(8;21) is distinguished from all other subtypes ,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_t(15;17),

5 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a positive fc value,

10 is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a negative fc value, and/or

15 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_inv(3),

and/or wherein

20 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is

25 distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a positive fc value,

30

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(15;17),

and/or wherein

5   a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(8;21),

10   and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a positive fc value,

15   is indicative for the presence of AML_inv(3) when AML_inv(3) is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a negative fc value, and/or

20   a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a positive fc value,

is indicative for the presence of AML_inv(3) when AML_inv(3) is distinguished from AML_t(15;17),

and/or wherein

25   a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a positive fc value,

is indicative for the presence of AML_inv(3) when AML_inv(3) is
30   distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a positive fc value,

is indicative for the presence of AML_normal when AML_normal is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a positive fc value,

is indicative for the presence of AML_normal when AML_normal is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a positive fc value,

is indicative for the presence of AML_t(15;17) when AML_t(15;17) is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.1 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from all other subtypes ,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.2 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.3 having a positive fc value,

is indicative for the presence of AML_inv(3) when AML_inv(3) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.4 having a positive fc value,

is indicative for the presence of AML_t(15;17) when AML_t(15;17) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 3.5 having a positive fc value,

is indicative for the presence of AML_t(8;21) when AML_t(8;21) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.1 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.2 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.3 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.4 having a positive fc value,

is indicative for the presence of AML_11q23 when AML_11q23 is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.5 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.6 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.7 having a positive fc value,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.8 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.8 having a positive fc value,

is indicative for the presence of AML_inv(3) when AML_inv(3) is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.9 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.9 having a positive fc value,

is indicative for the presence of AML_inv(3) when AML_inv(3) is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.10 having a negative fc value, and/or

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a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 4.10 having a positive fc value,

is indicative for the presence of AML_t(15;17)when AML_t(15;17)is distinguished from AML_t(8;21).

It has to be noted for clarification, that the data of Tables 1 and 2 consider the determination of AML with normal karyotype (AML_normal), whereas the data of Tables 3 and 4 do not consider the determination of AML with normal karyotype. As a consequence, a different gene expression profile between the analysis of Table 1/2 and 3/4 can be reflected.

As used herein, the following definitions apply to the above abbreviations:

AML_inv(3): AML with inversion 3

AML_t(8;21): AML with t(8;21) translocation

AML_t(15;17): AML with t(15;17) translocation

AML_inv(16): AML with inversion 16

AML_11q23: t(11q23)/MLL, AML with t(11q23) translocation on the mixed lineage leukaemia gene (MLL)

AML_normal: AML with normal karytype.

As used herein, "all other subtypes" refer to the subtypes of the present invention, the one which is under investigation versus the all others being included in the present invention.

According to the present invention, a "sample" means any biological material containing genetic information in the form of nucleic acids or proteins obtainable or obtained from an individual. The sample includes e.g. tissue samples, cell samples, bone marrow and/or body fluids such as blood, saliva, semen. Preferably, the sample is blood or bone marrow, more preferably the sample is bone marrow. The person skilled in the art is aware of methods, how to isolate nucleic acids and

proteins from a sample. A general method for isolating and preparing nucleic acids from a sample is outlined in Example 3.

5   According to the present invention, the term "lower expression" is generally assigned to all by numbers and Affymetrix Identification Numbers (ID). definable polynucleotides the t-values and fold change (fc) values of which are negative, as indicated in the Tables. Accordingly, the term "higher expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are positive.

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According to the present invention, the term "expression" refers to the process by which mRNA or a polypeptide is produced based on the nucleic acid sequence of a gene, i.e. „expression" also includes the formation of mRNA upon transcription. In accordance with the present invention, the term „determining the expression level"
15   preferably refers to the determination of the level of expression, namely of the markers.

Generally, "marker" refers to any genetically controlled difference which can be used in the genetic analysis of a test versus a control sample, for the purpose of
20   assigning the sample to a defined genotype or phenotype. As used herein, "markers" refer to genes which are differentially expressed in, e.g., different AML subtypes. The markers can be defined by their gene symbol name, their encoded protein name, their transcript identification number (cluster identification number), the data base accession number, public accession number or GenBank identifier or,
25   as done in the present invention, Affymetrix identification number, chromosomal location, UniGene accession number and cluster type, LocusLink accession number (see Examples and Tables).

The Affymetrix identification number (affy id) is accessible for anyone and the
30   person skilled in the art by entering the "gene expression omnibus" internet page of the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov/geo/). In particular, the affy id's of the polynucleotides used for the method of the present invention are derived from the

so-called U133 chip. The sequence data of each identification number can be viewed at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL96

Generally, the expression level of a marker is determined by the determining the expression of its corresponding "polynucleotide" as described hereinafter.

According to the present invention, the term „polynucleotide" refers, generally, to a DNA, in particular cDNA, or RNA, in particular a cRNA, or a portion thereof or a polypeptide or a portion thereof. In the case of RNA (or cDNA), the polynucleotide is formed upon transcription of a nucleotide sequence which is capable of expression. The polynucleotide fragments refer to fragments preferably of between at least 8, such as 10, 12, 15 or 18 nucleotides and at least 50, such as 60, 80, 100, 200 or 300 nucleotides in length, or a complementary sequence thereto, representing a consecutive stretch of nucleotides of a gene, cDNA or mRNA. In other terms, polynucleotides include also any fragment (or complementary sequence thereto) of a sequence derived from any of the markers defined above as long as these fragments unambiguously identify the marker.

The determination of the expression level may be effected at the transcriptional or translational level, i.e. at the level of mRNA or at the protein level. Protein fragments such as peptides or polypeptides advantageously comprise between at least 6 and at least 25, such as 30, 40, 80, 100 or 200 consecutive amino acids representative of the corresponding full length protein. Six amino acids are generally recognized as the lowest peptidic stretch giving rise to a linear epitope recognized by an antibody, fragment or derivative thereof. Alternatively, the proteins or fragments thereof may be analysed using nucleic acid molecules specifically binding to three-dimensional structures (aptamers).

Depending on the nature of the polynucleotide or polypeptide, the determination of the expression levels may be effected by a variety of methods. For determining and detecting the expression level, it is preferred in the present invention that the polynucleotide, in particular the cRNA, is labelled.

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The labelling of the polynucleotide or a polypeptide can occur by a variety of methods known to the skilled artisan. The label can be fluorescent, chemiluminescent, bioluminescent, radioactive (such as ^{3}H or ^{32}P). The labelling compound can be any labelling compound being suitable for the labelling of polynucleotides and/or polypeptides. Examples include fluorescent dyes, such as fluorescein, dichlorofluorescein, hexachlorofluorescein, BODIPY variants, ROX, tetramethylrhodamin, rhodamin X, Cyanine-2, Cyanine-3, Cyanine-5, Cyanine-7, IRD40, FluorX, Oregon Green, Alexa variants (available e.g. from Molecular Probes or Amersham Biosciences) and the like, biotin or biotinylated nucleotides, digoxigenin, radioisotopes, antibodies, enzymes and receptors. Depending on the type of labelling, the detection is done via fluorescence measurements, conjugation to streptavidin and/or avidin, antigen-antibody- and/or antibody-antibody-interactions, radioactivity measurements, as well as catalytic and/or receptor/ligand interactions. Suitable methods include the direct labelling (incorporation) method, the amino-modified (amino-allyl) nucleotide method (available e.g. from Ambion), and the primer tagging method (DNA dendrimer labelling, as kit available e.g. from Genisphere). Particularly preferred for the present invention is the use of biotin or biotinylated nucleotides for labelling, with the latter being directly incorporated into, e.g. the cRNA polynucleotide by in vitro transcription.

If the polynucleotide is mRNA, cDNA may be prepared into which a detectable label, as exemplified above, is incorporated. Said detectably labelled cDNA, in single-stranded form, may then be hybridised, preferably under stringent or highly stringent conditions to a panel of single-stranded oligonucleotides representing different genes and affixed to a solid support such as a chip. Upon applying appropriate washing steps, those cDNAs will be detected or quantitatively detected that have a counterpart in the oligonucleotide panel. Various advantageous embodiments of this general method are feasible. For example, the mRNA or the cDNA may be amplified e.g. by polymerase chain reaction, wherein it is preferable, for quantitative assessments, that the number of amplified copies corresponds relative to further amplified mRNAs or cDNAs to the number of mRNAs originally present in the cell. In a preferred embodiment of the present invention, the cDNAs are transcribed into cRNAs prior to the hybridisation step wherein only in the transcription step a label is incorporated into the nucleic acid and wherein the cRNA is employed for hybridisation. Alternatively, the label may be attached subsequent to the transcription step.

Similarly, proteins from a cell or tissue under investigation may be contacted with a panel of aptamers or of antibodies or fragments or derivatives thereof. The antibodies etc. may be affixed to a solid support such as a chip. Binding of proteins indicative of an AML subtype may be verified by binding to a detectably labelled secondary antibody or aptamer. For the labelling of antibodies, it is referred to Harlow and Lane, "Antibodies, a laboratory manual", CSH Press, 1988, Cold Spring Harbor. Specifically, a minimum set of proteins necessary for diagnosis of all AML subtypes may be selected for creation of a protein array system to make diagnosis on a protein lysate of a diagnostic bone marrow sample directly. Protein Array Systems for the detection of specific protein expression profiles already are available (for example: Bio-Plex, BIORAD, München, Germany). For this application preferably antibodies against the proteins have to be produced and immobilized on a platform e.g. glasslides or microtiterplates. The immobilized antibodies can be labelled with a reactant specific for the certain target proteins as discussed above. The reactants can include enzyme substrates, DNA, receptors, antigens or antibodies to create for example a capture sandwich immunoassay.

For reliably distinguishing AML subtypes it is useful that the expression of more than one of the above defined markers is determined. As a criterion for the choice of markers, the statistical significance of markers as expressed in q or p values based on the concept of the false discovery rate is determined. In doing so, a measure of statistical significance called the q value is associated with each tested feature. The q value is similar to the p value, except it is a measure of significance in terms of the false discovery rate rather than the false positive rate (Storey JD and Tibshirani R. Proc.Natl.Acad.Sci., 2003, Vol. 100:9440-5).

In a preferred embodiment of the present invention, markers as defined in Tables 1-4 having a q-value of less than 3E-06, more preferred less than 1.5E-09, most preferred less than 1.5E-11, less than 1.5E-20, less than 1.5E-30, are measured.

Of the above defined markers, the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of at least one of the Tables of the markers is determined.

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In another preferred embodiment, the expression level of at least 2, of at least 5, of at least 10 out of the markers having the numbers 1 – 10, 1-20, 1-40, 1-50 of at least one of the Tables are measured.

5   The level of the expression of the „marker", i.e. the expression of the polynucleotide is indicative of the AML subtype of a cell or an organism. The level of expression of a marker or group of markers is measured and is compared with the level of expression of the same marker or the same group of markers from other cells or samples. The comparison may be effected in an actual experiment or in

10   silico. When the expression level also referred to as expression pattern or expression signature (expression profile) is measurably different, there is according to the invention a meaningful difference in the level of expression. Preferably the difference at least is 5 %, 10% or 20%, more preferred at least 50% or may even be as high as 75% or 100%. More preferred the difference in the level of expression is

15   at least 200%, i.e. two fold, at least 500%, i.e. five fold, or at least 1000%, i.e. 10 fold.

Accordingly, the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least

20   5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype. On the other hand, the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%,

25   more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

In another embodiment of the present invention, the sample is derived from an

30   individual having leukaemia, preferably AML.

For the method of the present invention it is preferred if the polynucleotide the expression level of which is determined is in form of a transcribed polynucleotide. A particularly preferred transcribed polynucleotide is an mRNA, a cDNA and/or a

35   cRNA, with the latter being preferred. Transcribed polynucleotides are isolated from a sample, reverse transcribed and/or amplified, and labelled, by employing

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methods well-known the person skilled in the art (see Example 3). In a preferred embodiment of the methods according to the invention, the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.

5   In order to determine the expression level of the transcribed polynucleotide by the method of the present invention, it is preferred that the method comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions, as described hereinafter.

10   The term "hybridizing" means hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook, J., et al., in "Molecular Cloning: A Laboratory Manual" (1989), Eds. J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY and the further definitions provided above. Such
15   conditions are, for example, hybridization in 6x SSC, pH 7.0 / 0.1% SDS at about 45°C for 18-23 hours, followed by a washing step with 2x SSC/0.1% SDS at 50°C. In order to select the stringency, the salt concentration in the washing step can for example be chosen between 2x SSC/0.1% SDS at room temperature for low stringency and 0.2x SSC/0.1% SDS at 50°C for high stringency. In addition, the
20   temperature of the washing step can be varied between room temperature, ca. 22°C, for low stringency, and 65°C to 70° C for high stringency.Also contemplated are polynucleotides that hybridize at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation, preferably of formamide concentration
25   (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH2PO4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 mg/ml salmon sperm blocking DNA, followed by washes at 50°C with 1 X SSPE, 0.1%
30   SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5x SSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require
35   modification of the hybridization conditions described above, due to problems with compatibility.

"Complementary" and "complementarity", respectively, can be described by the percentage, i.e. proportion, of nucleotides which can form base pairs between two polynucleotide strands or within a specific region or domain of the two strands. Generally, complementary nucleotides are, according to the base pairing rules, adenine and thymine (or adenine and uracil), and cytosine and guanine. Complementarity may be partial, in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be a complete or total complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has effects on the efficiency and strength of hybridization between nucleic acid strands.

Two nucleic acid strands are considered to be 100% complementary to each other over a defined length if in a defined region all adenines of a first strand can pair with a thymine (or an uracil) of a second strand, all guanines of a first strand can pair with a cytosine of a second strand, all thymine (or uracils) of a first strand can pair with an adenine of a second strand, and all cytosines of a first strand can pair with a guanine of a second strand, and vice versa. According to the present invention, the degree of complementarity is determined over a stretch of 20, preferably 25, nucleotides, i.e. a 60% complementarity means that within a region of 20 nucleotides of two nucleic acid strands 12 nucleotides of the first strand can base pair with 12 nucleotides of the second strand according to the above ruling, either as a stretch of 12 contiguous nucleotides or interspersed by non-pairing nucleotides, when the two strands are attached to each other over said region of 20 nucleotides. The degree of complementarity can range from at least about 50% to full, i.e. 100% complementarity. Two single nucleic acid strands are said to be "substantially complementary" when they are at least about 80% complementary, preferably about 90% or higher. For carrying out the method of the present invention substantial complementarity is preferred.

Preferred methods for detection and quantification of the amount of polynucleotides, i.e. for the methods according to the invention allowing the determination of the level of expression of a marker, are those described by Sambrook et al. (1989) or real time methods known in the art as the TaqMan® method disclosed in WO92/02638 and the corresponding U.S. 5,210,015, U.S. 5,804,375, U.S. 5,487,972. This method exploits the exonuclease activity of a polymerase to generate a signal. In detail, the (at least one) target nucleic acid

component is detected by a process comprising contacting the sample with an oligonucleotide containing a sequence complementary to a region of the target nucleic acid component and a labeled oligonucleotide containing a sequence complementary to a second region of the same target nucleic acid component sequence strand, but not including the nucleic acid sequence defined by the first oligonucleotide, to create a mixture of duplexes during hybridization conditions, wherein the duplexes comprise the target nucleic acid annealed to the first oligonucleotide and to the labeled oligonucleotide such that the 3'-end of the first oligonucleotide is adjacent to the 5'-end of the labeled oligonucleotide. Then this mixture is treated with a template-dependent nucleic acid polymerase having a 5' to 3' nuclease activity under conditions sufficient to permit the 5' to 3' nuclease activity of the polymerase to cleave the annealed, labeled oligonucleotide and release labeled fragments. The signal generated by the hydrolysis of the labeled oligonucleotide is detected and/ or measured. TaqMan® technology eliminates the need for a solid phase bound reaction complex to be formed and made detectable. Other methods include e.g. fluorescence resonance energy transfer between two adjacently hybridized probes as used in the LightCycler® format described in U.S. 6,174,670.

A preferred protocol if the marker, i.e. the polynucleotide, is in form of a transcribed nucleotide, is described in Example 3, where total RNA is isolated, cDNA and, subsequently, cRNA is synthesized and biotin is incorporated during the transcription reaction. The purified cRNA is applied to commercially available arrays which can be obtained e.g. from Affymetrix. The hybridized cRNA is detected according to the methods described in Example 3. The arrays are produced by photolithography or other methods known to experts skilled in the art e.g. from U.S. 5,445,934, U.S. 5,744,305, U.S. 5,700,637, U.S. 5,945,334 and EP 0 619 321 or EP 0 373 203, or as decribed hereinafter in greater detail.

In another embodiment of the present invention, the polynucleotide or at least one of the polynucleotides is in form of a polypeptide. In another preferred embodiment, the expression level of the polynucleotides or polypeptides is detected using a compound which specifically binds to the polynucleotide of the polypeptide of the present invention.

As used herein, "specifically binding" means that the compound is capable of discriminating between two or more polynucleotides or polypeptides, i.e. it binds to the desired polynucleotide or polypeptide, but essentially does not bind unspecifically to a different polynucleotide or polypeptide.

5

The compound can be an antibody, or a fragment thereof, an enzyme, a so-called small molecule compound, a protein-scaffold, preferably an anticalin. In a preferred embodiment, the compound specifically binding to the polynucleotide or polypeptide is an antibody, or a fragment thereof.

10

As used herein, an "antibody" comprises monoclonal antibodies as first described by Köhler and Milstein in Nature 278 (1975), 495-497 as well as polyclonal antibodies, i.e. antibodies contained in a polyclonal antiserum. Monoclonal antibodies include those produced by transgenic mice. Fragments of antibodies

15   include F(ab')$_2$, Fab and Fv fragments. Derivatives of antibodies include scFvs, chimeric and humanized antibodies. See, for example Harlow and Lane, loc. cit. For the detection of polypeptides using antibodies or fragments thereof, the person skilled in the art is aware of a variety of methods, all of which are included in the present invention. Examples include immunoprecipitation, Western blotting,

20   Enzyme-linked immuno sorbent assay (ELISA), Enzyme-linked immuno sorbent assay (RIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFIA), scintillation proximity assay (SPA). For detection, it is desirable if the antibody is labelled by one of the labelling compounds and methods described supra.

25   In another preferred embodiment of the present invention, the method for distinguishing AML subtype AML_inv(3) from other AML subtypes, preferably from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal is carried out on an array.

30   In general, an "array" or "microarray" refers to a linear or two- or three dimensional arrangement of preferably discrete nucleic acid or polypeptide probes which comprises an intentionally created collection of nucleic acid or polypeptide probes of any length spotted onto a substrate/solid support. The person skilled in the art knows a collection of nucleic acids or polypeptide spotted onto a

35   substrate/solid support also under the term "array". As known to the person skilled

in the art, a microarray usually refers to a miniaturised array arrangement, with the probes being attached to a density of at least about 10, 20, 50, 100 nucleic acid molecules referring to different or the same genes per cm^2. Furthermore, where appropriate an array can be referred to as "gene chip". The array itself can have different formats, e.g. libraries of soluble probes or libraries of probes tethered to resin beads, silica chips, or other solid supports.

The process of array fabrication is well-known to the person skilled in the art. In the following, the process for preparing a nucleic acid array is described. Commonly, the process comprises preparing a glass (or other) slide (e.g. chemical treatment of the glass to enhance binding of the nucleic acid probes to the glass surface), obtaining DNA sequences representing genes of a genome of interest, and spotting sequences these sequences of interest onto glass slide. Sequences of interest can be obtained via creating a cDNA library from an mRNA source or by using publicly available databases, such as GeneBank, to annotate the sequence information of custom cDNA libraries or to identify cDNA clones from previously prepared libraries. Generally, it is recommendable to amplify obtained sequences by PCR in order to have sufficient amounts of DNA to print on the array. The liquid containing the amplified probes can be deposited on the array by using a set of microspotting pins. Ideally, the amount deposited should be uniform. The process can further include UV-crosslinking in order to enhance immobilization of the probes on the array.

In a preferred embodiment, the array is a high density oligonucleotide (oligo) array using a light-directed chemical synthesis process, employing the so-called photolithography technology. Unlike common cDNA arrays, oligo arrays (according to the Affymetrix technology) use a single-dye technology. Given the sequence information of the markers, the sequence can be synthesized directly onto the array, thus, bypassing the need for physical intermediates, such as PCR products, required for making cDNA arrays. For this purpose, the marker, or partial sequences thereof, can be represented by 14 to 20 features, preferably by less than 14 features, more preferably less than 10 features, even more preferably by 6 features or less, with each feature being a short sequence of nucleotides (oligonucleotide), which is a perfect match (PM) to a segment of the respective gene. The PM oligonucleotide are paired with mismatch (MM) oligonucleotides which have a single mismatch at the central base of the nucleotide and are used as "controls". The chip exposure sites are defined by masks and are deprotected by

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the use of light, followed by a chemical coupling step resulting in the synthesis of one nucleotide. The masking, light deprotection, and coupling process can then be repeated to synthesize the next nucleotide, until the nucleotide chain is of the specified length.

Advantageously, the method of the present invention is carried out in a robotics system including robotic plating and a robotic liquid transfer system, e.g. using microfluidics, i.e. channelled structured.

A particular preferred method according to the present invention is as follows:
1. Obtaining a sample, e.g. bone marrow aliquots, from a patient having AML
2. Extracting RNA, preferably mRNA, from the sample
3. Reverse transcribing the RNA into cDNA
4. In vitro transcribing the cDNA into cRNA
5. Fragmenting the cRNA
6. Hybridizing the fragmented cRNA on standard microarrays
7. Determining hybridization

In another embodiment, the present invention is directed to the use of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, and/or 4, for the manufacturing of a diagnostic for distinguishing AML subtype AML_inv(3) from other AML subtypes, preferably from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal. The use of the present invention is particularly advantageous for distinguishing AML subtype AML_inv(3) from other AML subtypes, preferably from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal in an individual having AML. The use of said markers for diagnosis of WHO classified leukemia subtypes, preferably based on microarray technology, offers the following advantages: (1) more rapid and more precise diagnosis, (2) easy to use in laboratories without specialized experience, (3) abolishes the requirement for analyzing viable cells for chromosome analysis (transport problem), and (4) very experienced hematologists for cytomorphology and cytochemistry, immunophenotyping as well as cytogeneticists and molecularbiologists are no longer required.

Accordingly, the present invention refers to a diagnostic kit containing at least one marker selected from the markers identifiable by their Affymetrix Identification

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Numbers (affy id) as defined in Tables 1, 2, 3, and/or 4, for distinguishing AML subtype AML_inv(3) from other AML subtypes, preferably from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal, in combination with suitable auxiliaries. Suitable auxiliaries, as used herein, include buffers, enzymes, labelling compounds, and the like. In a preferred embodiment, the marker contained in the kit is a nucleic acid molecule which is capable of hybridizing to the mRNA corresponding to at least one marker of the present invention. Preferably, the at least one nucleic acid molecule is attached to a solid support, e.g. a polystyrene microtiter dish, nitrocellulose membrane, glass surface or to non-immobilized particles in solution.

In another preferred embodiment, the diagnostic kit contains at least one reference for an AML subtype AML_inv(3) and/or any other AML subtype, preferably from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal. As used herein, the reference can be a sample or a data bank.

In another embodiment, the present invention is directed to an apparatus for distinguishing AML subtype AML_inv(3) from other AML subtypes, preferably from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal in a sample, containing a reference data bank obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, and/or 4 and

(b) classifying the gene expression profile by means of a machine learning algorithm.

According to the present invention, the "machine learning algorithm" is a computational-based prediction methodology, also known to the person skilled in the art as "classifier", employed for characterizing a gene expression profile. The signals corresponding to a certain expression level which are obtained by the microarray hybridization are subjected to the algorithm in order to classify the expression profile. Supervised learning involves "training" a classifier to recognize the distinctions among classes and then "testing" the accuracy of the classifier on an independent test set. For new, unknown samples the classifier shall predict into which class the sample belongs.

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Preferably, the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines (SVM), and Feed-Forward Neural Networks. Most preferably, the machine learning algorithm is Support Vector Machine, such as polynomial kernel and Gaussian Radial Basis Function-kernel SVM models.

The classification accuracy of a given gene list for a set of microarray experiments is preferably estimated using Support Vector Machines (SVM), because there is evidence that SVM-based prediction slightly outperforms other classification techniques like k-Nearest Neighbors (k-NN). The LIBSVM software package version 2.36 was used (SVM-type: C-SVC, linear kernel (http://www.csie.ntu.edu.tw/~cjlin/libsvm/)). The skilled artisan is furthermore referred to Brown et al., Proc.Natl.Acad.Sci., 2000; 97: 262-267, Furey et al., Bioinformatics. 2000; 16: 906-914, and Vapnik V. Statistical Learning Theory. New York: Wiley, 1998.

In detail, the classification accuracy of a given gene list for a set of microarray experiments can be estimated using Support Vector Machines (SVM) as supervised learning technique. Generally, SVMs are trained using differentially expressed genes which were identified on a subset of the data and then this trained model is employed to assign new samples to those trained groups from a second and different data set. Differentially expressed genes were identified applying ANOVA and t-test-statistics (Welch t-test). Based on identified distinct gene expression signatures respective training sets consisting of 2/3 of cases and test sets with 1/3 of cases to assess classification accuracies are designated. Assignment of cases to training and test set is randomized and balanced by diagnosis. Based on the training set a Support Vector Machine (SVM) model is built.

According to the present invention, the apparent accuracy, i.e. the overall rate of correct predictions of the complete data set was estimated by 10fold cross validation. This means that the data set was divided into 10 approximately equally sized subsets, an SVM-model was trained for 9 subsets and predictions were generated for the remaining subset. This training and prediction process was repeated 10 times to include predictions for each subset. Subsequently the data set was split into a training set, consisting of two thirds of the samples, and a test set

with the remaining one third. Apparent accuracy for the training set was estimated by 10fold cross validation (analogous to apparent accuracy for complete set). A SVM-model of the training set was built to predict diagnosis in the independent test set, thereby estimating true accuracy of the prediction model. This prediction approach was applied both for overall classification (multi-class) and binary classification (diagnosis X => yes or no). For the latter, sensitivity and specificity were calculated:

Sensitivity = (number of positive samples predicted)/(number of true positives)

Specificity = (number of negative samples predicted)/(number of true negatives)

In a preferred embodiment, the reference data bank is backed up on a computational data memory chip which can be inserted in as well as removed from the apparatus of the present invention, e.g. like an interchangeable module, in order to use another data memory chip containing a different reference data bank.

The apparatus of the present invention containing a desired reference data bank can be used in a way such that an unknown sample is, first, subjected to gene expression profiling, e.g. by microarray analysis in a manner as described supra or in the art, and the expression level data obtained by the analysis are, second, fed into the apparatus and compared with the data of the reference data bank obtainable by the above method. For this purpose, the apparatus suitably contains a device for entering the expression level of the data, for example a control panel such as a keyboard. The results, whether and how the data of the unknown sample fit into the reference data bank can be made visible on a provided monitor or display screen and, if desired, printed out on an incorporated of connected printer.

Alternatively, the apparatus of the present invention is equipped with particular appliances suitable for detecting and measuring the expression profile data and, subsequently, proceeding with the comparison with the reference data bank. In this embodiment, the apparatus of the present invention can contain a gripper arm and/or a tray which takes up the microarray containing the hybridized nucleic acids.

In another embodiment, the present invention refers to a reference data bank for distinguishing AML subtype AML_inv(3) from other AML subtypes, preferably

from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal in a sample obtainable by comprising

    (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, and/or 4, and

    (b) classifying the gene expression profile by means of a machine learning algorithm.

Preferably, the reference data bank is backed up and/or contained in a computational memory data chip.

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The invention is further illustrated in the following table and examples, without limiting the scope of the invention:

TABLES 1.1-4.10

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Tables 1.1-4.10 show AML subtype analysis of AML subtype AML_inv(3) and other AML subtypes, preferably from t(8;21), t(15;17), inv(16), t(11q23)/MLL, and/or AML_normal. The analysed markers are ordered according to their q-values, beginning with the lowest q-values.

10   For convenience and a better understanding, Tables 1.1 to 4.10 are accompanied with explanatory tables (Table 1.1A to 4.10A) where the numbering and the Affymetrix Id are further defined by other parameters, e.g. gene bank accession number.

15   **EXAMPLES**

Example 1:   General experimental design of the invention and results

The inv(3)(q21q26)/t(3;3)(q21;q26) can be found in about 1-2% of all unselected

20   AML and MDS RAEB-1 and RAEB-2. Although these 3q21q26 aberrations are correlated   with   characteristic   features   such   as   thrombocytosis, micromegakaryocytes, trilineage dysplasia, and with an unfavourable prognosis, they are not strictly correlated with an FAB subtype. The breakpoints in 3q21 as well as in 3q26 vary considerably at the molecular level. Long range activation of

25   the EVI1 gene, residing in 3q26, was reported to be involved in the pathogenetic mechanism of these AML. However, the pathophysiologic mechanisms of the 3q21q26 leukemia are poorly understood. Here we addressed the question, whether inv(3)/t(3;3) positive AML can be characterized by distinct gene expression patterns as recently demonstrated for other AML with balanced chromosomal

30   aberrations. Fifteen cases with 3q21q26 were hybridized onto the U133 set microarrays (Affymetrix) and compared to a cohort of 97 AML with other balanced chromosomal aberrations: t(8;21) (n=19), t(15;17) (n=20), inv(16) (n=24), t(11q23)/MLL (n=31), 132 AML with normal and 36 with complex aberrant karyotype. Distinct expression signatures accurately distinguish the

35   3q21q26 AML from all other AML subtypes with 100% accuracy, both by supervised and by unsupervised analysis. In fact, one of the differentially expressed genes was EVI1. Two different microarray probesets revealed absence of EVI1

expression in t(8;21), t(15;17), inv(16), and low or absent expression in normal and complex aberrant karyotypes. High expression was found in t(11q23)/MLL AML and even 4-fold higher in 3q21q26 leukemias. The EVI1 expression was confirmed with a real time LightCycler assay in all 3q21q26 AML and in 205 selected cases of all other groups. Both platforms reproducibly reveal a high correlation of EVI1 expression for both probesets (r=0.943 and r=0.767, respectively). The characteristic immunophenotype of 3q21q26 with high CD34+, low CD97+, low lactotransferrin+, and low MPO+ in comparison to all other subtypes could also be confirmed at the gene expression level. We then focussed on genes known to be involved in megakaryopoiesis. A higher expression of GATA1, GATA3, HOXC4, some genes for GP-proteins (GP1BA, GP1BB, GP5, and GP6) and IGHM was found in 3q21q26 leukemias but not in other AML. In addition, a high expression of PF4 (platelet factor 4) and its transactivator PBX2 was detected. Expression of TPO was not changed, but its receptor MPL was 6 fold upregulated in 3q21q26 AML in comparison to other AML. Moreover, upregulation of genes known to be targeted by mutations in some inborn platelet disorders were found: ETS1, FLI1, WAS, CBFA2T2 and CBFA2T3. As EVI1 was activated by a long range effect in 3q21q26 AML we further investigated genes located in the respective breakpoint regions. In fact many of them were dysregulated in comparison to other AML and normal bone marrow. For example in i) 3q21 high: MYLK, ITGB5, TRAD, MCM2, TM4SF1, ATP2C1, NCK1, WDR5B ii) 3q21 low: CSTA, SELB, WDR10 iii) 3q26 high: GOLPH4, PDCD10, KCNMB3 iv) 3q26 low: PLD1, FAD104. Thus, like EVI1 many genes in 3q21 and 3q26 may be affected by the 3q21q26 rearrangement, i.e. by long distance effect. In conclusion, the identification of new candidate genes associated with this subtype allows a better understanding of the pathogenesis of the 3q21q26 AML. The specific expression signature together with phenotypic characteristics showed that 3q21q26 AML is a biologically distinct subgroup. As such we suggest to add this subgroup to the WHO classification as an own entity .

Example 2: General materials, methods and definitions of functional annotations

The methods section contains both information on statistical analyses used for identification of differentially expressed genes and detailed annotation data of identified microarray probesets.

Affymetrix Probeset Annotation

All annotation data of GeneChip® arrays are extracted from the NetAffx™ Analysis Center (internet website: www.affymetrix.com). Files for U133 set arrays, including U133A and U133B microarrays are derived from the June 2003 release. The original publication refers to: Liu G, Loraine AE, Shigeta R, Cline M, Cheng J, Valmeekam V, Sun S, Kulp D, Siani-Rose MA. NetAffx: Affymetrix probesets and annotations. Nucleic Acids Res. 2003;31(1):82-6.

The sequence data are omitted due to their large size, and because they do not change, whereas the annotation data are updated periodically, for example new information on chromomal location and functional annotation of the respective gene products. Sequence data are available for download in the NetAffx Download Center (www.affymetrix.com)

Data fields:

In the following section, the content of each field of the data files are described. Microarray probesets, for example found to be differentially expressed between different types of leukemia samples are further described by additional information. The fields are of the following types:

1. GeneChip Array Information
2. Probe Design Information
3. Public Domain and Genomic References

1. GeneChip Array Information

HG-U133 ProbeSet_ID:

HG-U133 ProbeSet_ID describes the probe set identifier. Examples are: 200007_at, 200011_s_at, 200012_x_at.

GeneChip:

The description of the GeneChip probe array name where the respective probeset is represented. Examples are: Affymetrix Human Genome U133A Array or Affymetrix Human Genome U133B Array.

2. Probe Design Information

Sequence Type:

The Sequence Type indicates whether the sequence is an Exemplar, Consensus or Control sequence. An Exemplar is a single nucleotide sequence taken directly from a public database. This sequence could be an mRNA or EST. A Consensus sequence, is a nucleotide sequence assembled by Affymetrix, based on one or more sequence taken from a public database.

Transcript ID:

The cluster identification number with a sub-cluster identifier appended.

Sequence Derived From:

The accession number of the single sequence, or representative sequence on which the probe set is based. Refer to the "Sequence Source" field to determine the database used.

Sequence ID:

For Exemplar sequences: Public accession number or GenBank identifier. For Consensus sequences: Affymetrix identification number or public accession number.

Sequence Source:

The database from which the sequence used to design this probe set was taken. Examples are: GenBank®, RefSeq, UniGene, TIGR (annotations from The Institute for Genomic Research).

3. Public Domain and Genomic References

Most of the data in this section come from LocusLink and UniGene databases, and are annotations of the reference sequence on which the probe set is modeled.

Gene Symbol and Title:

A gene symbol and a short title, when one is available. Such symbols are assigned by different organizations for different species. Affymetrix annotational data come from the UniGene record. There is no indication which species-specific databank was used, but some of the possibilities include for example HUGO: The Human Genome Organization.

MapLocation:

The map location describes the chromosomal location when one is available.

5   Unigene_Accession:

UniGene accession number and cluster type. Cluster type can be "full length" or "est", or "---" if unknown.

LocusLink:

10   This information represents the LocusLink accession number.

Full Length Ref. Sequences:

Indicates the references to multiple sequences in RefSeq. The field contains the ID and description for each entry, and there can be multiple entries per probeSet.

15

Example 3:   Sample preparation, processing and data analysis

Method 1:

Microarray analyses were performed utilizing the GeneChip® System (Affymetrix,
20   Santa Clara, USA). Hybridization target preparations were performed according to recommended protocols (Affymetrix Technical Manual). In detail, at time of diagnosis, mononuclear cells were purified by Ficoll-Hypaque density centrifugation. They had been lysed immediately in RLT buffer (Qiagen, Hilden, Germany), frozen, and stored at -80°C from 1 week to 38 months. For gene
25   expression profiling cell lysates of the leukemia samples were thawed, homogenized (QIAshredder, Qiagen), and total RNA was extracted (RNeasy Mini Kit, Qiagen). Subsequently, 5-10 µg total RNA isolated from 1×10^7 cells was used as starting material for cDNA synthesis with oligo[(dT)$_{24}$T7promotor]$_{65}$ primer (cDNA Synthesis System, Roche Applied Science, Mannheim, Germany).
30   cDNA products were purified by phenol/chlorophorm/IAA extraction (Ambion, Austin, USA) and acetate/ethanol-precipitated overnight. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the following *in vitro* transcription reaction (Enzo BioArray HighYield RNA Transcript Labeling Kit, Enzo Diagnostics). After quantification by
35   spectrophotometric measurements and 260/280 absorbance values assessment for quality control of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 µg cRNA was

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fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2/500 mM potassium acetate/150 mM magnesium acetate) and added to the hybridization cocktail sufficient for five hybridizations on standard GeneChip microarrays (300 µl final volume). Washing and staining of the probe arrays was performed according to the recommended Fluidics Station protocol (EukGE-WS2v4). Affymetrix Microarray Suite software (version 5.0.1) extracted fluorescence signal intensities from each feature on the microarrays as detected by confocal laser scanning according to the manufacturer's recommendations.

Expression analysis quality assessment parameters included visiual array inspection of the scanned image for the presence of image artifacts and correct grid alignment for the identification of distinct probe cells as well as both low 3'/5' ratio of housekeeping controls (mean: 1.90 for GAPDH) and high percentage of detection calls (mean: 46.3% present called genes). The 3' to 5' ratio of GAPDH probesets can be used to assess RNA sample and assay quality. Signal values of the 3' probe sets for GAPDH are compared to the Signal values of the corresponding 5' probe set. The ratio of the 3' probe set to the 5' probe set is generally no more than 3.0. A high 3' to 5' ratio may indicate degraded RNA or inefficient synthesis of ds cDNA or biotinylated cRNA (GeneChip® Expression Analysis Technical Manual, www.affymetrix.com). Detection calls are used to determine whether the transcript of a gene is detected (present) or undetected (absent) and were calculated using default parameters of the Microarray Analysis Suite MAS 5.0 software package.

Method 2:
Bone marrow (BM) aspirates are taken at the time of the initial diagnostic biopsy and remaining material is immediately lysed in RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis. For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) is used. The targets for GeneChip analysis are prepared according to the current Expression Analysis. Briefly, frozen lysates of the leukemia samples are thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen).Normally 10 ug total RNA isolated from 1 x 107 cells is used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA is purified by phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For

- 34 -

detection of the hybridized target nucleic acid biotin-labeled ribonucleotides are incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug are fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) are chosen for monitoring of the integrity of the cRNA. Only labeled cRNA-cocktails which showed a ratio of the messured intensity of the 3' to the 5' end of the GAPDH gene less than 3.0 are selected for subsequent hybridization on HG-U133 probe arrays (Affymetrix). Washing and staining the Probe arrays is performed as described (siehe Affymetrix-Original-Literatur (LOCKHART und LIPSHUTZ). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the arrays as detected by confocal laser scanning according to the manufacturers recommendations.

Table 1

1. One-Versus-All (OVA)

1.1 11q23 versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205453_at	HOXB2	-9.16	5.54E-34	1.71E-29	-0.92	-14.34	17q21-q22
2	225344_at	ERAP140	-3.54	9.79E-33	1.51E-28	-0.91	-14.04	6q22.33
3	226517_at	BCAT1	-7.37	3.52E-29	3.64E-25	-0.83	-12.91	12pter-q12
4	200923_at	LGALS3BP	-7.42	7.40E-28	5.73E-24	-0.82	-12.60	17q25
5	202746_at	ITM2A	-7.88	1.46E-27	9.04E-24	-0.80	-12.43	Xq13.3-Xq21.2
6	236513_at		-2.80	1.45E-25	5.00E-22	-0.80	-12.18	
7	206761_at	TACTILE	-11.19	3.98E-26	2.05E-22	-0.78	-12.03	3q13.13
8	205624_at	CPA3	-12.31	6.26E-26	2.77E-22	-0.78	-11.99	3q21-q25
9	202747_s_at	ITM2A	-7.67	1.83E-25	5.65E-22	-0.77	-11.86	Xq13.3-Xq21.2
10	213258_at		-9.52	1.15E-25	4.44E-22	-0.77	-11.85	
11	211137_s_at	ATP2C1	-1.93	1.24E-23	2.96E-20	-0.79	-11.85	3q21-q24
12	228904_at		-9.68	9.09E-25	2.56E-21	-0.77	-11.69	
13	201830_s_at	NET1	-3.02	5.42E-22	9.87E-19	-0.79	-11.56	10p15
14	210664_s_at	TFPI	-6.02	2.08E-24	5.37E-21	-0.74	-11.43	2q31-q32.1
15	220306_at	FLJ20202	-3.65	3.19E-23	7.05E-20	-0.75	-11.41	1p11.1
16	221235_s_at		-2.09	8.31E-22	1.35E-18	-0.77	-11.41	
17	225831_at	LOC148894	-2.83	2.74E-20	3.39E-17	-0.78	-11.22	1p36.11
18	241756_at		-2.87	3.92E-18	2.86E-15	-0.81	-11.04	
19	214390_s_at	BCAT1	-5.82	2.42E-22	4.99E-19	-0.72	-10.96	12pter-q12
20	210993_s_at	MADH1	-5.11	7.86E-22	1.35E-18	-0.71	-10.86	4q28
21	205366_s_at	HOXB6	-15.75	4.15E-22	8.03E-19	-0.70	-10.78	17q21.3
22	221760_at	MAN1A1	-4.63	1.12E-21	1.73E-18	-0.69	-10.64	6q22
23	213549_at	PRO2730	-2.72	1.95E-20	2.51E-17	-0.70	-10.53	3p21.31
24	239791_at		-12.97	3.55E-21	5.24E-18	-0.68	-10.48	
25	201829_at	NET1	-2.10	1.65E-18	1.34E-15	-0.73	-10.47	10p15
26	210665_at	TFPI	-8.51	5.06E-21	7.13E-18	-0.67	-10.40	2q31-q32.1
27	236892_s_at		-11.68	9.17E-21	1.23E-17	-0.69	-10.40	
28	225285_at		-6.04	3.20E-19	3.19E-16	-0.70	-10.35	
29	224049_at	KCNK17	-2.52	1.71E-19	1.82E-16	-0.69	-10.32	6p21.1
30	242051_at		-3.10	4.34E-20	4.80E-17	-0.68	-10.32	
31	222920_s_at	KIAA0748	-4.32	2.34E-19	2.41E-16	-0.68	-10.25	12q13.13
32	201242_s_at	ATP1B1	-3.87	3.62E-18	2.73E-15	-0.70	-10.20	1q22-q25
33	219686_at	HSA250839	-6.75	3.92E-20	4.50E-17	-0.66	-10.12	4p16.2
34	219188_s_at	LRP16	-2.90	3.01E-18	2.33E-15	-0.69	-10.10	11q11
35	227297_at		-7.34	3.84E-20	4.50E-17	-0.65	-10.08	
36	233849_s_at	ARHGAP5	-5.80	9.16E-19	8.10E-16	-0.67	-10.07	14q12
37	208116_s_at	MAN1A1	-3.24	5.28E-19	4.95E-16	-0.67	-10.06	6q22

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
38	236198_at		-4.75	1.34E-18	1.12E-15	-0.67	-10.01	
39	225974_at	DKFZp762C1112	-4.33	8.06E-17	5.09E-14	-0.70	-9.97	8q21.3
40	218966_at	MYO5C	-2.12	2.38E-16	1.37E-13	-0.70	-9.86	15q21
41	226867_at	FLJ20686	-2.39	6.88E-19	6.26E-16	-0.65	-9.86	9p21.3
42	200829_x_at	ZNF207	-1.46	2.97E-14	1.12E-11	-0.78	-9.85	17q11.2
43	226342_at		-4.49	4.30E-19	4.16E-16	-0.64	-9.82	
44	203544_s_at	STAM	-2.52	3.50E-16	1.97E-13	-0.70	-9.79	10p14-p13
45	235142_at	MGC17919	-3.58	1.25E-18	1.08E-15	-0.63	-9.68	1p34.3
46	225830_at	LOC118987	-2.42	6.92E-18	4.87E-15	-0.63	-9.58	10q26.12
47	204951_at	ARHH	-2.95	3.86E-15	1.73E-12	-0.70	-9.54	4p13
48	241133_at	TRB	-5.63	1.93E-18	1.53E-15	-0.62	-9.54	7q34
49	243888_at		-2.64	8.83E-17	5.47E-14	-0.65	-9.50	
50	200953_s_at	CCND2	-2.64	5.88E-16	3.03E-13	-0.66	-9.46	12p13

1.2 inv(16) versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202370_s_at	CBFB	-2.72	4.30E-36	2.40E-32	-1.24	-18.06	16q22.1
2	227567_at		-4.70	1.45E-32	3.37E-29	-1.27	-17.96	
3	225055_at	DKFZp667M2411	-4.70	6.24E-34	1.74E-30	-1.25	-17.94	17q11.2
4	213737_x_at		-2.52	6.40E-37	4.46E-33	-1.12	-16.75	
5	214651_s_at	HOXA9	-14.42	4.42E-42	1.23E-37	-1.08	-16.73	7p15-p14
6	232636_at	DKFZp547M2010	-10.42	1.43E-39	1.99E-35	-1.04	-16.09	Xq27.3
7	235753_at		-8.08	3.36E-39	3.12E-35	-1.04	-15.99	
8	226352_at		-5.30	2.49E-34	7.71E-31	-1.00	-15.19	
9	209905_at	HOXA9	-42.52	5.18E-36	2.41E-32	-0.99	-15.12	7p15-p14
10	225102_at	LOC152009	-4.70	2.64E-32	5.66E-29	-1.00	-14.99	3q21.3
11	211031_s_at	CYLN2	-6.51	4.91E-35	1.96E-31	-0.95	-14.67	7q11.23
12	228497_at	FLIPT1	-4.94	2.40E-34	7.71E-31	-0.93	-14.48	1p13.1
13	223471_at	RAB3IP	-3.17	4.25E-25	3.48E-22	-1.01	-14.25	
14	219218_at	FLJ23058	-5.83	2.86E-33	7.25E-30	-0.92	-14.21	17q25.3
15	224952_at	DKFZP564D166	-3.66	6.61E-20	2.30E-17	-1.11	-14.20	17q23.3
16	206847_s_at	HOXA7	-4.55	2.66E-31	4.66E-28	-0.93	-14.15	7p15-p14
17	222786_at	C4S-2	-3.19	1.39E-31	2.78E-28	-0.91	-13.96	7p22
18	218414_s_at	NUDE1	-2.01	9.62E-25	7.25E-22	-0.97	-13.82	16p13.11
19	229215_at	ASCL2	-6.48	8.02E-31	1.32E-27	-0.90	-13.72	11p15.5
20	227224_at	FLJ25604	-4.55	3.91E-25	3.30E-22	-0.96	-13.70	1q24.2
21	201669_s_at	MARCKS	-10.42	2.68E-31	4.66E-28	-0.87	-13.52	6q22.2
22	200675_at	CD81	-3.13	1.13E-18	3.47E-16	-1.05	-13.35	11p15.5
23	213150_at	HOXA10	-6.78	1.59E-30	2.47E-27	-0.86	-13.32	7p15-p14
24	235521_at	HOXA3	-13.38	2.92E-30	4.28E-27	-0.87	-13.30	7p15-p14
25	230894_s_at		-8.98	6.25E-29	7.92E-26	-0.86	-13.14	
26	213779_at	LOC129080	-3.11	5.69E-27	6.35E-24	-0.88	-13.12	22q12.1
27	223044_at	SLC11A3	-7.75	1.88E-28	2.28E-25	-0.86	-13.08	2q32
28	217963_s_at	NGFRAP1	-10.36	3.75E-29	4.98E-26	-0.85	-13.06	Xq22.1
29	235391_at	LOC137392	-7.67	1.57E-29	2.19E-26	-0.84	-12.99	8q21.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
30	209406_at	BAG2	-3.60	1.47E-26	1.58E-23	-0.84	-12.70	6p12.3-p11.2
31	211026_s_at	MGLL	-2.54	3.79E-24	2.71E-21	-0.84	-12.45	3q21.3
32	241706_at	LOC144402	-5.02	1.29E-25	1.20E-22	-0.82	-12.36	12q11
33	200985_s_at	CD59	-6.42	3.05E-26	3.15E-23	-0.81	-12.35	11p13
34	226817_at		-5.26	3.78E-27	4.39E-24	-0.80	-12.31	
35	241985_at	FLJ37870	-5.40	3.83E-25	3.30E-22	-0.82	-12.31	5q13.3
36	201432_at	CAT	-2.02	1.25E-16	2.77E-14	-0.99	-12.30	11p13
37	213353_at	ABCA5	-3.06	9.05E-18	2.32E-15	-0.94	-12.22	17q24.3
38	216920_s_at	TRGV9	-4.25	3.65E-25	3.28E-22	-0.80	-12.12	7p15
39	200984_s_at	CD59	-3.07	2.15E-23	1.25E-20	-0.81	-12.04	11p13
40	218477_at	PTD011	-2.68	3.02E-21	1.34E-18	-0.84	-12.02	6p12.1
41	220668_s_at	DNMT3B	-2.83	5.32E-24	3.54E-21	-0.80	-11.99	20q11.2
42	219304_s_at	SCDGF-B	-2.99	8.28E-26	8.25E-23	-0.78	-11.97	11q22.3
43	218795_at	ACP6	-3.21	1.17E-18	3.56E-16	-0.88	-11.89	1q21
44	204197_s_at	RUNX3	-2.89	8.95E-24	5.67E-21	-0.79	-11.88	1p36
45	213908_at		-5.96	1.15E-25	1.11E-22	-0.76	-11.82	
46	215806_x_at	TRGC2	-3.94	1.04E-23	6.30E-21	-0.78	-11.77	7p15
47	213241_at		-3.73	4.96E-25	3.95E-22	-0.76	-11.71	
48	213147_at	HOXA10	-3.83	6.75E-21	2.65E-18	-0.81	-11.69	7p15-p14
49	235749_at	UGCGL2	-4.91	9.42E-24	5.84E-21	-0.77	-11.63	13q32.1
50	213002_at	MARCKS	-3.08	8.04E-25	6.23E-22	-0.75	-11.60	6q22.2

1.3 inv(3) versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205382_s_at	DF	-5.92	8.32E-28	1.98E-23	-1.12	-15.98	19p13.3
2	230480_at	HIWI2	-3.35	1.38E-21	4.70E-18	-0.86	-12.44	11q21
3	204647_at	HOMER3	-4.67	4.41E-22	2.09E-18	-0.79	-11.77	19p13.11
4	210115_at	RPL39L	-6.00	3.06E-25	3.63E-21	-0.75	-11.69	3q27
5	204301_at	KIAA0711	-6.79	7.34E-25	5.81E-21	-0.76	-11.68	8p23.2
6	223703_at	CDA017	-2.62	1.91E-15	1.97E-12	-0.86	-11.38	10q23.1
7	204082_at	PBX3	-4.18	2.02E-20	5.34E-17	-0.76	-11.22	9q33-q34
8	213110_s_at	COL4A5	-11.30	4.39E-23	2.61E-19	-0.71	-11.03	Xq22
9	212318_at	TRN-SR	-2.17	1.20E-11	3.52E-09	-0.97	-11.02	7q32.2
10	231300_at	LOC90835	-2.80	2.55E-13	1.35E-10	-0.88	-11.01	16p11.2
11	204548_at	STAR	-6.67	1.21E-21	4.70E-18	-0.70	-10.78	8p11.2
12	212953_x_at	CALR	-2.13	1.05E-20	3.12E-17	-0.71	-10.75	19p13.3-p13.2
13	226789_at		-2.38	1.36E-12	5.86E-10	-0.87	-10.66	
14	214575_s_at	AZU1	-5.42	8.17E-16	9.25E-13	-0.77	-10.61	19p13.3
15	202759_s_at	AKAP2	-2.93	7.67E-14	5.21E-11	-0.81	-10.54	9q31-q33
16	204921_at	GAS8	-2.67	2.30E-19	4.55E-16	-0.71	-10.52	16q24.3
17	200700_s_at	KDELR2	-2.21	1.60E-12	6.66E-10	-0.84	-10.39	7p22.2
18	201186_at	LRPAP1	-2.60	6.43E-15	5.87E-12	-0.76	-10.39	4p16.3
19	205767_at	EREG	-7.12	4.02E-20	8.69E-17	-0.68	-10.35	4q21.1
20	205624_at	CPA3	-6.98	2.71E-20	6.45E-17	-0.67	-10.27	3q21-q25

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
21	242621_at	FLJ32468	-1.46	3.56E-12	1.25E-09	-0.82	-10.15	7q22.1
22	203746_s_at	HCCS	-1.50	6.88E-17	9.62E-14	-0.70	-10.11	Xp22.3
23	208967_s_at	AK2	-2.29	8.09E-15	6.63E-12	-0.70	-9.76	1p34
24	205131_x_at	SCGF	-4.79	2.56E-16	3.21E-13	-0.66	-9.69	19q13.3
25	236892_s_at		-7.73	8.30E-19	1.52E-15	-0.62	-9.66	
26	213893_x_at	PMS2L5	-1.89	1.14E-09	1.70E-07	-0.90	-9.64	7q11-q22
27	213844_at	HOXA5	-5.15	5.19E-15	5.14E-12	-0.68	-9.58	7p15-p14
28	226123_at	LOC286180	-3.22	2.00E-12	8.04E-10	-0.74	-9.58	8q12.1
29	218865_at	FLJ22390	-6.90	3.52E-18	5.98E-15	-0.61	-9.46	1q42.11
30	232250_at	KIAA1257	-3.08	6.20E-13	2.95E-10	-0.69	-9.34	3q21.3
31	235077_at		-3.90	2.97E-17	4.42E-14	-0.61	-9.28	
32	239791_at		-6.95	1.33E-17	2.11E-14	-0.60	-9.27	
33	217499_x_at		-1.53	9.73E-12	3.04E-09	-0.72	-9.23	
34	231736_x_at	MGST1	-3.33	1.39E-09	1.99E-07	-0.84	-9.22	12p12.3-p12.1
35	228161_at	RAB32	-1.74	1.42E-13	8.46E-11	-0.66	-9.18	6q24.2
36	210783_x_at	SCGF	-4.49	1.60E-14	1.23E-11	-0.64	-9.18	19q13.3
37	239656_at		-2.09	3.79E-12	1.31E-09	-0.70	-9.17	
38	227929_at		-6.47	1.67E-16	2.20E-13	-0.60	-9.15	
39	210006_at	DKFZP564O243	-1.70	4.60E-11	1.07E-08	-0.73	-9.14	3p21.1
40	223534_s_at	RPS6KL1	-1.78	5.76E-10	9.50E-08	-0.79	-9.12	14q24.2
41	203675_at	NUCB2	-2.23	6.37E-10	1.04E-07	-0.79	-9.08	11p15.1-p14
42	228293_at	LOC91614	-4.40	3.58E-11	8.69E-09	-0.72	-9.04	11p13
43	243917_at		-1.39	1.17E-12	5.25E-10	-0.66	-8.95	
44	211048_s_at	ERP70	-2.09	6.36E-12	2.16E-09	-0.67	-8.93	7q35
45	226556_at		-2.59	6.68E-10	1.08E-07	-0.76	-8.90	
46	203421_at	PIG11	-3.06	7.66E-16	9.10E-13	-0.58	-8.88	11p11.2
47	231415_at	WBSCR22	-2.61	7.66E-15	6.63E-12	-0.60	-8.85	
48	240672_at		-1.45	2.71E-12	1.00E-09	-0.65	-8.82	
49	219588_s_at	FLJ20311	-2.22	1.23E-10	2.47E-08	-0.71	-8.80	7q36.3
50	204332_s_at	AGA	-1.66	1.23E-11	3.57E-09	-0.66	-8.78	4q32-q33

1.4 normal versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205600_x_at	HOXB5	2.30	6.96E-29	1.51E-24	0.95	13.64	17q21.3
2	205601_s_at	HOXB5	3.09	6.49E-27	7.07E-23	0.94	13.15	17q21.3
3	228904_at		8.93	8.57E-26	5.91E-22	1.04	13.10	
4	236892_s_at		17.81	3.14E-24	9.76E-21	1.05	12.54	
5	205366_s_at	HOXB6	15.23	1.24E-24	5.41E-21	0.94	12.52	17q21.3
6	239791_at		15.87	3.58E-24	9.76E-21	1.02	12.50	
7	205453_at	HOXB2	3.87	1.09E-25	5.91E-22	0.79	12.06	17q21-q22
8	231767_at	HOXB4	2.86	2.89E-24	9.76E-21	0.82	11.92	17q21-q22
9	230743_at		2.18	2.42E-21	5.27E-18	0.79	11.06	
10	229194_at		1.97	3.15E-22	7.62E-19	0.70	10.78	

11	219304_s_at	SCDGF-B	2.56	2.92E-20	5.77E-17	0.71	10.45 11q22.3
12	216973_s_at	HOXB7	3.97	7.64E-18	1.39E-14	0.75	9.91 17q21.3
13	213110_s_at	COL4A5	5.14	2.76E-17	4.29E-14	0.67	9.52 Xq22
14	204779_s_at	HOXB7	4.49	8.50E-17	1.16E-13	0.71	9.48 17q21.3
15	238058_at		2.13	2.42E-17	4.06E-14	0.62	9.34
16	232424_at	PRDM16	10.27	2.89E-16	3.50E-13	0.74	9.32 1p36.23-p33
17	235749_at	UGCGL2	2.82	7.12E-17	1.03E-13	0.60	9.13 13q32.1
18	240151_at		1.88	9.18E-17	1.18E-13	0.59	9.04
19	201427_s_at	SEPP1	4.63	9.91E-16	1.14E-12	0.60	8.84 5q31
20	225362_at	LOC159090	1.36	1.45E-15	1.57E-12	0.55	8.55 Xq26.3
21	232979_at		2.78	1.08E-14	9.43E-12	0.60	8.51
22	AFFX-HSAC07/X00351_M_at - HG-U133B	ACTB	-1.58	2.93E-15	3.04E-12	-0.55	-8.49 7p15-p12
23	225971_at		1.64	4.26E-15	4.22E-12	0.54	8.40
24	209406_at	BAG2	2.17	5.62E-15	5.32E-12	0.54	8.36 6p12.3-p11.2
25	209112_at	CDKN1B	1.58	9.51E-15	8.63E-12	0.53	8.27 12p13.1-p12
26	AFFX-HSAC07/X00351_5_at - HG-U133A	ACTB	-1.81	3.02E-14	2.35E-11	-0.54	-8.19 7p15-p12
27	207111_at	EMR1	2.82	5.08E-14	3.59E-11	0.56	8.19 19p13.3
28	209679_s_at	LOC57228	-2.09	5.11E-14	3.59E-11	-0.55	-8.18 12q13.12
29	217848_s_at	PP	1.58	2.02E-14	1.69E-11	0.53	8.16 10q11.1-q24
30	233467_s_at	PHEMX	1.47	2.53E-14	2.04E-11	0.53	8.14 11p15.5
31	203591_s_at	CSF3R	-2.02	2.29E-13	1.26E-10	-0.58	-8.10 1p35-p34.3
32	200740_s_at	SMT3H1	1.30	3.78E-14	2.84E-11	0.52	8.07 21q22.3
33	238498_at		2.45	5.81E-14	3.96E-11	0.53	8.06
34	AFFX-HSAC07/X00351_5_at - HG-U133B	ACTB	-1.80	8.12E-14	5.36E-11	-0.53	-8.03 7p15-p12
35	204778_x_at	HOXB7	3.06	1.66E-13	1.01E-10	0.55	8.00 17q21.3
36	240180_at		1.78	1.13E-13	7.05E-11	0.53	7.98
37	AFFX-HSAC07/X00351_M_at - HG-U133A	ACTB	-1.53	8.49E-14	5.44E-11	-0.51	-7.95 7p15-p12
38	243010_at	MSI2	2.13	3.15E-13	1.61E-10	0.54	7.90 17q23.1
39	200696_s_at	GSN	-1.75	4.44E-13	2.06E-10	-0.54	-7.88 9q33
40	224773_at	NAV1	-2.86	1.42E-12	5.52E-10	-0.59	-7.86
41	204785_x_at	IFNAR2	1.56	1.79E-13	1.05E-10	0.51	7.85 21q22.11
42	241464_s_at		1.93	1.95E-13	1.12E-10	0.51	7.84
43	240131_at		1.89	2.31E-13	1.26E-10	0.50	7.79
44	228571_at		1.59	2.90E-13	1.54E-10	0.50	7.75
45	235587_at	LOC202781	1.63	4.63E-13	2.10E-10	0.51	7.74 7q36.3
46	218258_at	RPAC2	1.32	3.26E-13	1.61E-10	0.50	7.73 13q12.13
47	213353_at	ABCA5	1.69	3.20E-13	1.61E-10	0.50	7.72 17q24.3
48	238778_at	FLJ32798	3.05	4.72E-13	2.10E-10	0.51	7.72 10p11.1
49	235331_x_at		1.69	3.33E-13	1.61E-10	0.50	7.72
50	201664_at	SMC4L1	1.66	3.95E-13	1.87E-10	0.50	7.71 3q26.1

1.5 t(15;17) versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	-9.63	6.57E-58	4.20E-54	-1.57	-23.80	6p21.3
2	204425_at	ARHGAP4	-16.60	6.18E-64	1.19E-59	-1.51	-23.49	Xq28
3	209732_at	CLECSF2	-25.48	7.22E-60	6.93E-56	-1.46	-22.47	12p13-p12
4	213587_s_at	LOC155066	-5.51	5.76E-55	2.76E-51	-1.35	-20.92	7q36.1
5	205771_s_at	AKAP7	-10.27	1.00E-53	3.86E-50	-1.36	-20.88	6q23
6	213147_at	HOXA10	-14.75	3.38E-51	1.08E-47	-1.26	-19.48	7p15-p14
7	201923_at	PRDX4	-5.89	7.32E-35	4.53E-32	-1.35	-19.35	Xp22.13
8	217848_s_at	PP	-4.03	5.52E-28	1.31E-25	-1.41	-18.97	10q11.1-q24
9	214651_s_at	HOXA9	-136.34	3.00E-47	8.23E-44	-1.25	-18.66	7p15-p14
10	204362_at	SCAP2	-12.68	5.38E-47	1.29E-43	-1.21	-18.60	7p21-p15
11	241742_at	PRAM-1	-6.74	6.92E-45	1.21E-41	-1.18	-18.17	19p13.2
12	201719_s_at	EPB41L2	-10.75	1.09E-45	2.32E-42	-1.15	-17.87	6q23
13	201137_s_at	HLA-DPB1	-9.36	1.40E-45	2.70E-42	-1.15	-17.84	6p21.3
14	204563_at	SELL	-6.03	7.71E-39	8.70E-36	-1.19	-17.83	1q23-q25
15	225639_at	SCAP2	-10.70	2.18E-39	2.62E-36	-1.19	-17.78	7p21-p15
16	200931_s_at	VCL	-3.68	3.04E-28	7.48E-26	-1.25	-17.32	10q22.1-q23
17	228113_at	STAT3	-4.16	3.36E-27	6.90E-25	-1.26	-17.30	17q21
18	203948_s_at	MPO	3.42	7.87E-17	3.92E-15	1.62	17.17	17q23.1
19	216899_s_at	SCAP2	-6.04	2.37E-38	2.29E-35	-1.10	-16.64	7p21-p15
20	227598_at	LOC113763	-4.11	2.06E-33	1.04E-30	-1.12	-16.53	7q35
21	217478_s_at	HLA-DMA	-5.05	1.58E-32	7.14E-30	-1.12	-16.45	6p21.3
22	235753_at		-9.53	1.82E-40	2.91E-37	-1.07	-16.39	
23	214797_s_at	PCTK3	-4.71	2.20E-25	3.49E-23	-1.20	-16.36	1q31-q32
24	232617_at	CTSS	-5.24	2.36E-40	3.49E-37	-1.06	-16.34	1q21
25	213150_at	HOXA10	-26.84	4.98E-40	6.37E-37	-1.06	-16.28	7p15-p14
26	212953_x_at	CALR	3.48	4.59E-13	1.32E-11	2.30	16.20	19p13.3-p13.2
27	236322_at		-6.02	1.85E-29	5.00E-27	-1.13	-16.19	
28	211991_s_at	HLA-DPA1	-14.16	2.90E-40	3.98E-37	-1.04	-16.18	6p21.3
29	236554_x_at	EVER2	-3.49	4.34E-23	5.41E-21	-1.22	-16.09	17q25.3
30	204361_s_at	SCAP2	-8.90	1.49E-34	8.51E-32	-1.07	-16.04	7p21-p15
31	221004_s_at	ITM2C	5.98	3.40E-13	9.98E-12	2.13	16.03	2q37
32	209448_at	HTATIP2	-6.94	2.39E-38	2.29E-35	-1.03	-15.85	11p15.1
33	229041_s_at		-23.25	2.21E-38	2.29E-35	-1.03	-15.78	
34	214450_at	CTSW	7.22	1.11E-12	2.97E-11	2.39	15.77	11q13.1
35	227353_at	EVER2	-3.52	4.10E-20	3.55E-18	-1.26	-15.77	17q25.3
36	225386_s_at	LOC92906	-19.67	3.32E-38	3.03E-35	-1.01	-15.62	2p22.2
37	210145_at	PLA2G4A	-6.27	6.85E-37	5.47E-34	-1.02	-15.60	1q25
38	211474_s_at	SERPINB6	-3.83	3.38E-30	1.01E-27	-1.07	-15.55	6p25
39	205453_at	HOXB2	-12.69	6.60E-38	5.76E-35	-1.01	-15.54	17q21-q22

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
40	201753_s_at	ADD3	-5.38	1.92E-30	6.23E-28	-1.06	-15.53	10q24.2-q24.3
41	238949_at	FLJ31951	-7.08	3.38E-32	1.44E-29	-1.04	-15.51	5q33.3
42	209905_at	HOXA9	-361.44	4.48E-37	3.74E-34	-1.04	-15.49	7p15-p14
43	208306_x_at	HLA-DRB4	-6.23	2.87E-28	7.16E-26	-1.07	-15.43	6p21.3
44	230264_s_at	AP1S2	-5.32	5.62E-36	4.15E-33	-1.00	-15.38	Xp22.31
45	206847_s_at	HOXA7	-5.99	1.90E-34	1.04E-31	-1.01	-15.36	7p15-p14
46	209312_x_at	HLA-DRB1	-5.91	9.96E-27	1.80E-24	-1.08	-15.32	6p21.3
47	200654_at	P4HB	2.22	2.38E-14	8.36E-13	1.58	15.26	17q25
48	38487_at	STAB1	8.02	2.26E-12	5.70E-11	2.35	15.23	3p21.31
49	203949_at	MPO	2.36	5.16E-19	3.78E-17	1.23	15.21	17q23.1
50	203299_s_at	AP1S2	-4.02	2.19E-31	8.24E-29	-1.02	-15.14	Xp22.31

1.6 t(8;21) versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	-119.43	4.83E-47	1.40E-42	-1.24	-18.57	7p15-p14
2	221581_s_at	WBSCR5	-5.89	1.92E-42	1.86E-38	-1.17	-17.78	7q11.23
3	213147_at	HOXA10	-9.51	2.99E-43	4.35E-39	-1.14	-17.48	7p15-p14
4	225615_at	LOC126917	-6.42	9.85E-38	3.58E-34	-1.12	-16.85	1p36.13
5	213150_at	HOXA10	-32.72	2.09E-40	1.52E-36	-1.07	-16.40	7p15-p14
6	235753_at		-8.55	2.77E-39	1.61E-35	-1.03	-15.94	
7	215087_at		-3.53	5.35E-37	1.63E-33	-1.04	-15.84	
8	205453_at	HOXB2	-14.60	1.66E-38	8.05E-35	-1.02	-15.71	17q21-q22
9	206847_s_at	HOXA7	-5.31	6.33E-38	2.63E-34	-1.02	-15.71	7p15-p14
10	209905_at	HOXA9	-314.99	5.62E-37	1.63E-33	-1.03	-15.44	7p15-p14
11	226865_at		-5.92	1.20E-35	3.17E-32	-0.95	-14.82	
12	224764_at	ARHGAP10	-5.16	4.47E-31	7.65E-28	-0.99	-14.79	10
13	204494_s_at	DKFZP434H132	-2.99	1.64E-29	2.52E-26	-0.98	-14.58	15q22.33
14	238077_at	MGC27385	-3.63	6.81E-28	7.92E-25	-0.99	-14.51	3p21.1
15	204069_at	MEIS1	-11.83	1.42E-33	3.19E-30	-0.93	-14.29	2p14-p13
16	217963_s_at	NGFRAP1	-14.47	1.40E-33	3.19E-30	-0.92	-14.20	Xq22.1
17	204495_s_at	DKFZP434H132	-2.85	3.29E-29	4.55E-26	-0.94	-14.09	15q22.33
18	227279_at	MGC15737	-2.56	1.66E-18	5.95E-16	-1.09	-13.93	Xq22.1
19	201425_at	ALDH2	-6.63	2.09E-31	4.05E-28	-0.90	-13.86	12q24.2
20	241370_at		-3.00	8.73E-27	9.76E-24	-0.94	-13.79	
21	213844_at	HOXA5	-11.73	1.36E-31	2.82E-28	-0.88	-13.60	7p15-p14
22	235521_at	HOXA3	-16.52	4.29E-31	7.65E-28	-0.89	-13.59	7p15-p14
23	206310_at	SPINK2	-44.78	9.85E-31	1.59E-27	-0.89	-13.50	4q12
24	208890_s_at	PLXNB2	-3.59	3.80E-22	2.30E-19	-0.95	-13.35	22q13.33
25	208091_s_at	DKFZP564K0822	-5.01	1.98E-24	1.64E-21	-0.91	-13.26	7p14.1
26	203017_s_at	SSX2IP	-3.40	2.78E-22	1.76E-19	-0.93	-13.11	
27	209500_x_at	TNFSF13	-3.21	6.68E-24	5.25E-21	-0.90	-13.05	17p13.1
28	238455_at		-3.93	1.88E-28	2.28E-25	-0.85	-13.04	
29	228365_at	LOC144402	-6.68	2.03E-29	2.95E-26	-0.83	-12.95	12q11

30 206120_at	CD33	-4.08	1.19E-25	1.15E-22	-0.86	-12.81	19q13.3
31 227995_at		-7.24	1.13E-28	1.50E-25	-0.83	-12.79	
32 233955_x_at	HSPC195	-2.89	1.70E-24	1.45E-21	-0.86	-12.75	5q31.3
33 208146_s_at	CPVL	-12.53	1.82E-28	2.28E-25	-0.82	-12.67	7p15-p14
34 243806_at		-3.96	1.45E-25	1.36E-22	-0.84	-12.63	
35 203680_at	PRKAR2B	-5.25	4.03E-26	4.34E-23	-0.83	-12.57	7q22-q31.1
36 210314_x_at	TNFSF13	-3.71	1.67E-20	7.82E-18	-0.87	-12.25	17p13.1
37 236297_at		-3.21	9.86E-26	9.89E-23	-0.80	-12.16	
38 224516_s_at	HSPC195	-2.91	1.46E-24	1.29E-21	-0.78	-11.91	5q31.3
39 240572_s_at		-3.33	2.37E-19	9.42E-17	-0.85	-11.90	
40 213908_at		-5.85	8.32E-26	8.63E-23	-0.77	-11.87	
41 227276_at	TEM7R	-2.80	1.50E-20	7.13E-18	-0.83	-11.85	10p12.1
42 224049_at	KCNK17	-2.57	1.14E-24	1.03E-21	-0.77	-11.75	6p21.1
43 222996_s_at	HSPC195	-2.31	5.41E-23	3.83E-20	-0.79	-11.75	5q31.3
44 227853_at		-2.88	4.65E-15	7.56E-13	-0.94	-11.73	
45 220974_x_at	BA108L7.2	-4.10	7.98E-18	2.42E-15	-0.86	-11.69	10q24.31
46 225245_x_at	H2AFJ	-3.55	2.11E-19	8.66E-17	-0.83	-11.66	12p12
47 217226_s_at	BA108L7.2	-2.93	4.27E-17	1.05E-14	-0.87	-11.65	10q24.31
48 201951_at	ALCAM	-3.93	8.41E-20	3.60E-17	-0.81	-11.60	3q13.1
49 230894_s_at		-5.85	1.11E-22	7.53E-20	-0.77	-11.60	
50 223398_at	MGC11115	-2.54	1.74E-16	3.95E-14	-0.88	-11.57	9q22.2

Table 2

2. All-Pairs (AP)

2.1   11q23 versus inv(16)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1 213737_x_at			3.73	1.13E-15	1.73E-11	2.10	13.96	
2 200665_s_at	SPARC		-16.71	3.03E-13	1.32E-09	-2.29	-13.74	5q31.3-q32
3 200953_s_at	CCND2		-4.22	1.13E-15	1.73E-11	-1.89	-13.24	12p13
4 214651_s_at	HOXA9		24.48	6.34E-14	4.83E-10	2.09	12.83	7p15-p14
5 202746_at	ITM2A		-15.51	1.87E-12	5.21E-09	-2.15	-12.76	Xq13.3-Xq21.2
6 202747_s_at	ITM2A		-15.29	3.80E-12	7.25E-09	-2.03	-12.22	Xq13.3-Xq21.2
7 231310_at			-4.48	1.13E-14	1.15E-10	-1.64	-11.74	
8 200951_s_at	CCND2		-5.06	4.26E-13	1.63E-09	-1.72	-11.64	12p13
9 202551_s_at	CRIM1		-4.41	2.93E-13	1.32E-09	-1.63	-11.30	2p21
10 206847_s_at	HOXA7		6.89	1.31E-12	4.43E-09	1.67	10.96	7p15-p14
11 227567_at			5.37	2.91E-13	1.32E-09	1.58	10.93	
12 201497_x_at	MYH11		-25.07	1.61E-10	1.34E-07	-2.11	-10.83	16p13.13-p13.12
13 205453_at	HOXB2		-7.71	7.13E-12	1.28E-08	-1.64	-10.82	17q21-q22
14 235753_at			13.56	9.87E-12	1.51E-08	1.80	10.62	
15 201496_x_at	MYH11		-6.90	6.26E-11	7.35E-08	-1.73	-10.60	16p13.13-

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
								p13.12
16	212667_at	SPARC	-8.20	5.65E-11	6.89E-08	-1.65	-10.40	5q31.3-q32
17	224049_at	KCNK17	-4.41	9.00E-11	9.46E-08	-1.66	-10.31	6p21.1
18	213147_at	HOXA10	6.19	3.53E-12	7.19E-09	1.50	10.20	7p15-p14
19	229215_at	ASCL2	10.61	2.45E-11	3.40E-08	1.55	9.93	11p15.5
20	203949_at	MPO	-3.22	2.23E-12	5.29E-09	-1.38	-9.79	17q23.1
21	209905_at	HOXA9	81.21	7.73E-11	8.74E-08	1.69	9.76	7p15-p14
22	226517_at	BCAT1	-10.39	6.14E-10	3.82E-07	-1.62	-9.66	12pter-q12
23	202931_x_at	BIN1	-2.97	2.31E-12	5.29E-09	-1.32	-9.58	2q14
24	213908_at		15.53	1.14E-10	1.10E-07	1.59	9.54	
25	201830_s_at	NET1	-4.02	1.63E-10	1.34E-07	-1.45	-9.52	10p15
26	223471_at	RAB3IP	3.55	8.58E-12	1.45E-08	1.35	9.50	
27	201029_s_at	CD99	-1.93	2.43E-12	5.29E-09	-1.31	-9.48	Xp22.32
28	224952_at	DKFZP564D166	3.54	1.88E-12	5.21E-09	1.27	9.31	17q23.3
29	204082_at	PBX3	5.48	1.81E-10	1.45E-07	1.49	9.25	9q33-q34
30	228058_at	LOC124220	-5.44	9.13E-12	1.47E-08	-1.27	-9.16	16p13.3
31	225831_at	LOC148894	-3.50	2.57E-10	1.96E-07	-1.35	-9.05	1p36.11
32	205330_at	MN1	-16.11	4.51E-09	1.52E-06	-1.71	-9.04	22q12.1
33	202370_s_at	CBFB	3.04	1.34E-10	1.20E-07	1.36	9.03	16q22.1
34	225102_at	LOC152009	5.50	1.44E-10	1.26E-07	1.34	8.98	3q21.3
35	210139_s_at	PMP22	-8.84	3.42E-09	1.26E-06	-1.52	-8.92	17p12-p11.2
36	211012_s_at	PML	-2.72	4.71E-11	5.99E-08	-1.22	-8.76	15q22
37	200602_at	APP	-6.17	1.23E-10	1.14E-07	-1.24	-8.73	21q21.3
38	203733_at	MYLE	3.27	8.06E-11	8.78E-08	1.24	8.72	16p13.2
39	228496_s_at	CRIM1	-2.82	1.15E-10	1.10E-07	-1.23	-8.70	2p21
40	226137_at		-3.57	2.49E-09	1.07E-06	-1.38	-8.69	
41	214452_at	BCAT1	-4.11	1.17E-09	6.73E-07	-1.30	-8.60	12pter-q12
42	203329_at	PTPRM	-5.80	7.33E-09	2.17E-06	-1.48	-8.60	18p11.2
43	241706_at	LOC144402	6.03	4.36E-10	2.96E-07	1.26	8.52	12q11
44	213150_at	HOXA10	11.20	1.28E-09	7.06E-07	1.38	8.51	7p15-p14
45	201828_x_at	CXX1	2.80	1.75E-11	2.54E-08	1.15	8.51	Xq26
46	202265_at	BMI1	3.17	4.25E-10	2.95E-07	1.25	8.48	10p11.23
47	210006_at	DKFZP564O243	2.23	5.26E-10	3.42E-07	1.26	8.46	3p21.1
48	225285_at		-9.01	3.35E-09	1.26E-06	-1.31	-8.44	
49	242738_s_at		-2.35	5.69E-10	3.62E-07	-1.22	-8.43	
50	218966_at	MYO5C	-2.93	2.74E-09	1.13E-06	-1.28	-8.36	15q21

2.2 11q23 versus inv(3)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204082_at	PBX3	8.05	2.96E-11	4.56E-07	1.56	9.79	9q33-q34
2	226789_at		3.17	7.24E-11	4.56E-07	1.31	8.77	
3	225344_at	ERAP140	-4.35	2.49E-07	4.83E-05	-1.77	-8.74	6q22.33
4	214651_s_at	HOXA9	4.34	4.49E-11	4.56E-07	1.28	8.67	7p15-p14

5	222982_x_at	SLC38A2	-1.93	7.96E-10	1.84E-06	-1.31	-8.55 12q
6	213893_x_at	PMS2L5	2.34	7.87E-11	4.56E-07	1.26	8.53 7q11-q22
7	236398_s_at		6.39	2.46E-10	1.12E-06	1.29	8.52
8	235753_at		4.79	2.97E-10	1.12E-06	1.27	8.39
9	233955_x_at	HSPC195	-4.27	9.34E-09	6.01E-06	-1.34	-8.38 5q31.3
10	210006_at	DKFZP564O243	2.30	3.38E-10	1.12E-06	1.26	8.35 3p21.1
11	235199_at		-3.81	2.13E-07	4.41E-05	-1.54	-8.32
12	203733_at	MYLE	2.89	5.18E-10	1.33E-06	1.22	8.12 16p13.2
13	212318_at	TRN-SR	2.59	4.46E-10	1.29E-06	1.21	8.10 7q32.2
14	202053_s_at	ALDH3A2	2.81	1.73E-09	2.56E-06	1.22	7.94 17p11.2
15	214643_x_at	BIN1	-4.34	2.80E-07	5.15E-05	-1.43	-7.94 2q14
16	209905_at	HOXA9	6.89	1.61E-09	2.56E-06	1.21	7.93 7p15-p14
17	228083_at	CACNA2D4	8.25	1.77E-09	2.56E-06	1.21	7.91 12p13.33
18	225386_s_at	LOC92906	6.11	1.05E-09	2.22E-06	1.17	7.84 2p22.2
19	223703_at	CDA017	3.76	3.59E-09	3.24E-06	1.21	7.80 10q23.1
20	200602_at	APP	-9.73	7.82E-07	1.01E-04	-1.48	-7.75 21q21.3
21	212782_x_at	POLR2J	2.42	3.77E-09	3.24E-06	1.15	7.66 7q11.2
22	208116_s_at	MAN1A1	-4.72	9.63E-07	1.16E-04	-1.47	-7.63 6q22
23	208967_s_at	AK2	3.86	8.89E-09	5.89E-06	1.21	7.62 1p34
24	215667_x_at	PMS2L5	1.93	2.43E-09	3.01E-06	1.13	7.62 7q11-q22
25	225389_at	BTBD6	2.27	1.62E-09	2.56E-06	1.12	7.60 14q32
26	221036_s_at	PSFL	2.03	1.74E-09	2.56E-06	1.12	7.57 15q21.3
27	214430_at	GLA	2.10	2.07E-09	2.82E-06	1.11	7.51 Xq22
28	206440_at	LIN7A	8.97	8.85E-09	5.89E-06	1.16	7.49 12q21
29	230051_at		-4.16	5.08E-07	7.64E-05	-1.32	-7.48
30	209836_x_at	MGC5178	2.05	2.47E-09	3.01E-06	1.10	7.47 16p12.1
31	202961_s_at	ATP5J2	2.24	5.44E-09	4.35E-06	1.11	7.45 7q22.1
32	212174_at	AK2	3.70	6.56E-09	4.90E-06	1.13	7.45 1p34
33	213370_s_at	SFMBT	1.98	3.04E-09	3.24E-06	1.10	7.44 3p21.31
34	222996_s_at	HSPC195	-4.05	7.45E-07	9.81E-05	-1.34	-7.43 5q31.3
35	202054_s_at	ALDH3A2	4.23	2.86E-09	3.24E-06	1.09	7.42 17p11.2
36	224516_s_at	HSPC195	-5.00	2.99E-07	5.38E-05	-1.26	-7.41 5q31.3
37	206847_s_at	HOXA7	2.83	3.35E-09	3.24E-06	1.10	7.41 7p15-p14
38	201186_at	LRPAP1	3.21	7.87E-09	5.70E-06	1.12	7.39 4p16.3
39	219126_at	XAP135	1.82	3.30E-09	3.24E-06	1.09	7.38 6q27
40	219991_at	SLC2A9	2.18	5.75E-09	4.44E-06	1.11	7.38 4p16-p15.3
41	202605_at	GUSB	3.16	4.47E-09	3.70E-06	1.10	7.37 7q21.11
42	213908_at		3.92	1.51E-08	8.34E-06	1.15	7.37
43	223207_x_at	PHP14	1.80	3.42E-09	3.24E-06	1.09	7.36 9q34.3
44	220924_s_at	SLC38A2	-1.62	3.76E-09	3.24E-06	-1.08	-7.34 12q
45	200654_at	P4HB	2.25	8.68E-09	5.89E-06	1.09	7.28 17q25
46	206478_at	KIAA0125	-13.74	3.61E-06	2.61E-04	-1.64	-7.27 14q32.33
47	218041_x_at	SLC38A2	-1.65	1.58E-08	8.49E-06	-1.09	-7.21 12q
48	214453_s_at	IFI44	-4.71	1.66E-06	1.59E-04	-1.34	-7.18 1p31.1
49	231300_at	LOC90835	3.98	2.03E-08	9.99E-06	1.11	7.18 16p11.2
50	209696_at	FBP1	4.25	3.05E-08	1.29E-05	1.14	7.17 9q22.3

2.3 11q23 versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205453_at	HOXB2	-12.20	1.96E-35	5.87E-31	-1.29	-16.31	17q21-q22
2	228904_at		-14.32	2.38E-27	3.57E-23	-1.15	-13.75	
3	205366_s_at	HOXB6	-23.99	1.76E-25	1.76E-21	-1.06	-12.92	17q21.3
4	239791_at		-19.84	1.54E-24	1.16E-20	-1.03	-12.55	
5	236892_s_at		-17.98	3.08E-24	1.85E-20	-1.05	-12.52	
6	205601_s_at	HOXB5	-3.14	1.36E-22	6.80E-19	-0.92	-11.60	17q21.3
7	231767_at	HOXB4	-3.47	1.23E-21	5.25E-18	-0.91	-11.40	17q21-q22
8	211137_s_at	ATP2C1	-1.99	9.13E-21	3.43E-17	-0.85	-10.86	3q21-q24
9	200923_at	LGALS3BP	-8.71	4.82E-20	1.45E-16	-0.89	-10.81	17q25
10	225344_at	ERAP140	-3.36	1.70E-20	5.67E-17	-0.84	-10.72	6q22.33
11	213258_at		-9.54	6.33E-20	1.73E-16	-0.85	-10.64	
12	220306_at	FLJ20202	-3.46	1.84E-19	4.61E-16	-0.82	-10.41	1p11.1
13	210664_s_at	TFPI	-6.33	4.23E-19	9.07E-16	-0.82	-10.30	2q31-q32.1
14	236513_at		-2.70	3.53E-19	8.15E-16	-0.80	-10.23	
15	205600_x_at	HOXB5	-1.84	1.63E-18	3.26E-15	-0.79	-10.03	17q21.3
16	222920_s_at	KIAA0748	-4.54	2.86E-18	5.36E-15	-0.79	-9.96	12q13.13
17	210993_s_at	MADH1	-5.23	9.34E-18	1.65E-14	-0.76	-9.69	4q28
18	232424_at	PRDM16	-14.39	5.25E-17	8.29E-14	-0.80	-9.63	1p36.23-p33
19	205624_at	CPA3	-10.95	7.38E-17	1.11E-13	-0.77	-9.52	3q21-q25
20	226517_at	BCAT1	-6.15	3.45E-17	5.75E-14	-0.74	-9.49	12pter-q12
21	200829_x_at	ZNF207	-1.49	8.06E-15	6.36E-12	-0.80	-9.45	17q11.2
22	225974_at	DKFZp762C1112	-4.61	2.88E-16	3.75E-13	-0.75	-9.39	8q21.3
23	216973_s_at	HOXB7	-3.64	1.06E-16	1.51E-13	-0.74	-9.37	17q21.3
24	241756_at		-2.73	1.95E-15	2.02E-12	-0.77	-9.35	
25	210665_at	TFPI	-9.20	2.00E-16	2.72E-13	-0.75	-9.33	2q31-q32.1
26	227680_at	LOC284695	-2.04	5.14E-15	4.67E-12	-0.76	-9.20	1p22.1
27	221235_s_at		-2.05	4.09E-16	4.91E-13	-0.72	-9.11	
28	228974_at		-3.16	3.51E-16	4.39E-13	-0.71	-9.10	
29	226508_at		-1.73	1.54E-15	1.71E-12	-0.71	-8.94	
30	225223_at		-2.15	8.69E-15	6.68E-12	-0.72	-8.90	
31	244103_at		-2.08	2.99E-14	1.91E-11	-0.73	-8.88	
32	213549_at	PRO2730	-2.68	1.66E-15	1.77E-12	-0.69	-8.85	3p21.31
33	226867_at	FLJ20686	-2.48	1.53E-15	1.71E-12	-0.69	-8.85	9p21.3
34	233849_s_at	ARHGAP5	-6.23	2.02E-15	2.02E-12	-0.69	-8.81	14q12
35	208116_s_at	MAN1A1	-2.89	6.12E-15	5.12E-12	-0.70	-8.79	6q22
36	232979_at		-3.41	2.76E-15	2.67E-12	-0.69	-8.76	
37	243888_at		-2.66	5.90E-15	5.12E-12	-0.70	-8.76	
38	223298_s_at	NT5C3	-1.70	3.69E-15	3.46E-12	-0.69	-8.76	7p14.3
39	230743_at		-2.09	1.03E-14	7.76E-12	-0.70	-8.75	
40	219094_at	HSPC056	-2.10	1.34E-14	9.64E-12	-0.71	-8.75	3q22.3

41 229519_at	FXR1	-2.12	1.35E-14	9.64E-12	-0.70	-8.71	3q28
42 203544_s_at	STAM	-2.56	1.71E-14	1.17E-11	-0.70	-8.68	10p14-p13
43 227259_at	CD47	-1.62	2.50E-13	1.27E-10	-0.73	-8.63	3q13.1-q13.2
44 221760_at	MAN1A1	-3.82	6.14E-15	5.12E-12	-0.68	-8.62	6q22
45 231870_s_at	CGI-07	-1.64	1.76E-12	6.07E-10	-0.76	-8.60	3q26.1
46 236251_at		-3.32	1.66E-14	1.16E-11	-0.68	-8.59	
47 236198_at		-5.13	7.84E-15	6.36E-12	-0.67	-8.58	
48 201242_s_at	ATP1B1	-3.70	1.88E-14	1.25E-11	-0.68	-8.58	1q22-q25
49 225406_at	TWSG1	-2.25	1.18E-12	4.41E-10	-0.74	-8.55	18p11.3
50 204951_at	ARHH	-3.11	4.67E-14	2.86E-11	-0.68	-8.48	4p13

2.4   11q23 versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1 221004_s_at	ITM2C	-11.20	1.59E-14	7.61E-11	-2.87	-17.09	2q37
2 38487_at	STAB1	-16.01	3.30E-13	5.91E-10	-2.90	-16.10	3p21.31
3 203948_s_at	MPO	-6.05	4.56E-20	1.14E-15	-2.14	-15.28	17q23.1
4 205624_at	CPA3	-35.38	6.12E-12	5.68E-09	-3.00	-14.74	3q21-q25
5 212953_x_at	CALR	-3.21	1.82E-14	7.61E-11	-2.20	-14.27	19p13.3-p13.2
6 214450_at	CTSW	-6.21	4.49E-14	1.36E-10	-2.19	-14.03	11q13.1
7 200953_s_at	CCND2	-6.31	2.30E-12	2.80E-09	-2.26	-13.45	12p13
8 214651_s_at	HOXA9	234.13	3.24E-14	1.16E-10	2.39	13.42	7p15-p14
9 203949_at	MPO	-4.22	1.85E-17	2.31E-13	-1.87	-13.25	17q23.1
10 238022_at		-6.27	2.35E-12	2.80E-09	-1.99	-12.44	
11 206871_at	ELA2	-4.10	1.64E-16	1.37E-12	-1.75	-12.43	19p13.3
12 233072_at	KIAA1857	-12.50	6.74E-11	3.12E-08	-2.26	-12.31	9q34
13 213147_at	HOXA10	23.75	2.86E-13	5.88E-10	2.04	12.19	7p15-p14
14 201029_s_at	CD99	-2.27	1.40E-15	8.79E-12	-1.62	-11.54	Xp22.32
15 204150_at	STAB1	-19.83	3.61E-10	1.14E-07	-2.25	-11.52	3p21.31
16 206847_s_at	HOXA7	9.16	4.76E-13	7.95E-10	1.78	11.45	7p15-p14
17 210788_s_at	retSDR4	-2.58	1.11E-11	8.39E-09	-1.79	-11.35	14q22.3
18 209448_at	HTATIP2	10.11	1.01E-12	1.58E-09	1.80	11.31	11p15.1
19 200951_s_at	CCND2	-7.13	1.97E-10	7.68E-08	-1.93	-11.10	12p13
20 205663_at	PCBP3	-3.88	3.71E-11	1.90E-08	-1.79	-11.09	21q22.3
21 212509_s_at		-6.33	1.39E-10	6.21E-08	-1.87	-11.03	
22 206761_at	TACTILE	-25.65	1.23E-09	2.84E-07	-2.20	-10.83	3q13.13
23 235753_at		16.24	7.41E-12	6.19E-09	1.86	10.77	
24 231736_x_at	MGST1	-2.95	1.27E-13	2.89E-10	-1.53	-10.74	12p12.3-p12.1
25 213587_s_at	LOC155066	7.68	8.23E-12	6.65E-09	1.74	10.58	7q36.1
26 224918_x_at	MGST1	-2.77	4.90E-14	1.36E-10	-1.49	-10.57	12p12.3-p12.1
27 201596_x_at	KRT18	-9.08	5.27E-10	1.50E-07	-1.81	-10.49	12q13
28 205349_at	GNA15	-3.93	1.96E-12	2.73E-09	-1.53	-10.47	19p13.3
29 217848_s_at	PP	3.79	3.05E-13	5.88E-10	1.50	10.44	10q11.1-q24

# affy id	HUGO name	fc	p	q	stn	t	Map Location
30 201522_x_at	SNRPN	4.60	7.40E-14	1.85E-10	1.46	10.39	15q12
31 205771_s_at	AKAP7	9.76	6.69E-12	5.78E-09	1.62	10.38	6q23
32 200952_s_at	CCND2	-3.93	2.46E-10	8.91E-08	-1.67	-10.25	12p13
33 225532_at	LOC91768	-5.23	7.13E-10	1.88E-07	-1.73	-10.17	18q11.1
34 225386_s_at	LOC92906	35.64	2.81E-11	1.67E-08	1.73	10.16	2p22.2
35 221253_s_at	MGC3178	-3.09	1.65E-10	7.12E-08	-1.61	-10.14	6p24.3
36 218404_at	SNX10	6.55	1.28E-11	9.41E-09	1.55	10.03	7p15.2
37 204425_at	ARHGAP4	15.70	3.11E-11	1.80E-08	1.63	9.99	Xq28
38 204082_at	PBX3	8.58	2.56E-11	1.66E-08	1.58	9.93	9q33-q34
39 209905_at	HOXA9	701.37	6.10E-11	2.94E-08	1.77	9.88	7p15-p14
40 217716_s_at	SEC61A1	-1.97	6.02E-12	5.68E-09	-1.43	-9.86	3q21.3
41 213571_s_at	EIF4EL3	2.56	1.14E-12	1.67E-09	1.41	9.85	2q37.1
42 225570_at	SLC41A1	3.46	2.26E-12	2.80E-09	1.41	9.81	1q32.1
43 223663_at	FLJ37970	7.30	4.86E-12	5.07E-09	1.41	9.71	11q12.3
44 241383_at		-4.20	3.65E-09	6.44E-07	-1.74	-9.68	
45 219837_s_at	C17	-67.10	8.83E-09	1.18E-06	-2.02	-9.65	4p16-p15
46 210140_at	CST7	-6.71	1.39E-09	3.08E-07	-1.61	-9.65	20p11.21
47 208852_s_at	CANX	-2.25	6.37E-11	3.01E-08	-1.43	-9.58	5q35
48 216417_x_at	HOXB9	3.56	4.25E-12	4.63E-09	1.38	9.57	17q21.3
49 212813_at	JAM3	-4.92	4.22E-09	7.05E-07	-1.69	-9.54	11q25
50 202746_at	ITM2A	-18.16	8.43E-09	1.14E-06	-1.85	-9.52	Xq13.3-Xq21.2

2.5   11q23 versus t(8;21)

# affy id	HUGO name	fc	p	q	stn	t	Map Location
1 214651_s_at	HOXA9	206.03	3.28E-14	1.03E-09	2.38	13.41	7p15-p14
2 221581_s_at	WBSCR5	9.58	9.94E-14	1.56E-09	1.98	12.37	7q11.23
3 213147_at	HOXA10	15.43	4.12E-13	3.22E-09	1.91	11.80	7p15-p14
4 206847_s_at	HOXA7	8.17	9.28E-13	5.26E-09	1.83	11.41	7p15-p14
5 235753_at		14.64	8.54E-12	2.97E-08	1.82	10.68	
6 201105_at	LGALS1	6.65	1.61E-12	7.21E-09	1.54	10.34	22q13.1
7 227853_at		3.55	1.68E-13	1.76E-09	1.47	10.30	
8 209905_at	HOXA9	614.03	6.13E-11	1.37E-07	1.77	9.87	7p15-p14
9 203949_at	MPO	-3.89	1.01E-12	5.26E-09	-1.40	-9.82	17q23.1
10 210314_x_at	TNFSF13	4.55	4.40E-12	1.72E-08	1.42	9.72	17p13.1
11 213908_at		15.54	1.15E-10	2.13E-07	1.61	9.55	
12 213150_at	HOXA10	54.55	2.66E-10	3.78E-07	1.61	9.25	7p15-p14
13 209500_x_at	TNFSF13	3.85	4.68E-11	1.22E-07	1.37	9.17	17p13.1
14 204082_at	PBX3	6.31	5.89E-11	1.37E-07	1.34	9.03	9q33-q34
15 205639_at	AOAH	5.46	8.40E-11	1.75E-07	1.29	8.80	7p14-p12
16 228365_at	LOC144402	7.86	5.32E-10	6.36E-07	1.42	8.80	12q11
17 208890_s_at	PLXNB2	3.97	9.29E-11	1.82E-07	1.29	8.76	22q13.33
18 228083_at	CACNA2D4	12.54	7.21E-10	7.06E-07	1.44	8.75	12p13.33
19 201944_at	HEXB	3.38	5.49E-10	6.36E-07	1.39	8.72	5q13
20 218404_at	SNX10	4.18	1.56E-10	2.65E-07	1.29	8.68	7p15.2
21 204202_at	KIAA1023	3.42	1.65E-10	2.65E-07	1.28	8.66	7p22.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
22	225245_x_at	H2AFJ	4.99	2.65E-10	3.78E-07	1.30	8.64	12p12
23	212459_x_at	SUCLG2	3.67	2.89E-11	9.04E-08	1.22	8.63	3p14.2
24	216417_x_at	HOXB9	3.30	4.27E-11	1.22E-07	1.21	8.51	17q21.3
25	223562_at	PARVG	3.18	5.28E-10	6.36E-07	1.25	8.36	22q13.2-q13
26	218217_at	RISC	5.15	1.01E-09	8.75E-07	1.29	8.35	17q23.1
27	203948_s_at	MPO	-4.44	6.12E-10	6.61E-07	-1.23	-8.34	17q23.1
28	228058_at	LOC124220	-6.10	5.49E-09	3.37E-06	-1.29	-8.28	16p13.3
29	241706_at	LOC144402	5.35	8.09E-10	7.45E-07	1.22	8.17	12q11
30	201850_at	CAPG	7.89	3.15E-09	2.10E-06	1.35	8.17	2cen-q24
31	224301_x_at	H2AFJ	4.16	7.21E-10	7.06E-07	1.21	8.17	12p12
32	214835_s_at	SUCLG2	3.91	4.04E-10	5.27E-07	1.19	8.16	3p14.2
33	206940_s_at	POU4F1	-33.65	1.84E-07	3.22E-05	-1.76	-8.14	13q21.1-q22
34	212423_at	FLJ90798	5.61	1.08E-09	9.14E-07	1.22	8.14	10q22.3
35	215772_x_at	SUCLG2	3.87	1.69E-10	2.65E-07	1.15	8.09	3p14.2
36	202746_at	ITM2A	-7.27	5.70E-08	1.67E-05	-1.39	-8.08	Xq13.3-Xq21.2
37	238756_at		4.09	1.20E-09	9.93E-07	1.21	8.08	
38	204880_at	MGMT	-2.32	5.45E-09	3.37E-06	-1.23	-8.04	10q26
39	241370_at		3.17	2.09E-09	1.49E-06	1.20	7.94	
40	224415_s_at	HINT2	2.05	3.49E-10	4.75E-07	1.13	7.93	9p13.1
41	228827_at		-103.62	2.83E-07	4.30E-05	-1.80	-7.92	
42	225386_s_at	LOC92906	6.59	6.59E-10	6.88E-07	1.14	7.90	2p22.2
43	200788_s_at	PEA15	2.38	7.77E-10	7.37E-07	1.14	7.87	1q21.1
44	207839_s_at	LOC51754	2.68	5.92E-10	6.61E-07	1.12	7.85	9p13.1
45	206009_at	ITGA9	-3.62	5.12E-08	1.58E-05	-1.28	-7.81	3p21.3
46	211341_at	POU4F1	-150.84	3.58E-07	5.05E-05	-1.74	-7.79	13q21.1-q22
47	56256_at	CGI-40	2.81	1.88E-09	1.37E-06	1.14	7.77	11q23.3
48	217520_x_at	LOC283683	16.90	1.17E-08	5.50E-06	1.38	7.76	15q11.2
49	219478_at	WFDC1	-6.75	1.65E-07	3.09E-05	-1.36	-7.72	16q24.3
50	205774_at	F12	3.18	1.69E-09	1.32E-06	1.11	7.68	5q33-qter

2.6   inv(16) versus inv(3)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	4.74	1.72E-13	4.54E-09	2.41	14.22	17q23.1
2	203948_s_at	MPO	5.13	2.36E-12	2.08E-08	1.89	11.46	17q23.1
3	205382_s_at	DF	5.65	1.05E-12	1.38E-08	1.83	11.19	19p13.3
4	201497_x_at	MYH11	18.46	2.05E-10	7.07E-07	2.06	10.65	16p13.13-p13.12
5	224841_x_at		-1.69	2.14E-10	7.07E-07	-1.76	-10.33	
6	224741_x_at		-1.69	3.09E-10	9.08E-07	-1.76	-10.28	
7	209365_s_at	ECM1	3.28	3.37E-11	2.23E-07	1.54	9.53	1q21
8	210755_at	HGF	6.18	6.96E-10	1.84E-06	1.65	9.44	7q21.1
9	228497_at	FLIPT1	-3.11	8.82E-09	1.17E-05	-1.63	-9.19	1p13.1
10	205718_at	ITGB7	3.07	1.91E-10	7.07E-07	1.44	8.88	12q13.13

11	205131_x_at	SCGF	4.37	1.79E-10	7.07E-07	1.40	8.73 19q13.3
12	217963_s_at	NGFRAP1	-20.39	5.19E-07	1.67E-04	-1.88	-8.49 Xq22.1
13	201496_x_at	MYH11	3.64	1.43E-09	3.16E-06	1.40	8.45 16p13.13-p13.12
14	222862_s_at	AK5	40.65	3.10E-08	2.93E-05	1.61	8.14 1p31
15	236646_at	FLJ31166	3.02	9.63E-10	2.31E-06	1.30	8.12 12p13.31
16	226197_at		2.75	2.51E-09	4.46E-06	1.31	8.04
17	203074_at	ANXA8	1.80	2.08E-09	4.22E-06	1.30	8.04 10q11.2
18	243244_at		3.90	2.53E-09	4.46E-06	1.29	7.95
19	202605_at	GUSB	2.22	4.26E-08	3.47E-05	1.30	7.70 7q21.11
20	212358_at	CLIPR-59	15.49	8.58E-08	5.04E-05	1.46	7.63 19q13.12
21	201360_at	CST3	3.63	4.80E-09	7.94E-06	1.22	7.62 20p11.21
22	226697_at	LOC92689	2.52	6.69E-09	1.04E-05	1.22	7.58 4p14
23	201462_at	KIAA0193	-5.29	3.06E-07	1.13E-04	-1.37	-7.57 7p14.3-p14.1
24	241525_at	LOC200772	55.36	1.35E-07	6.48E-05	1.47	7.46 2q37.3
25	210783_x_at	SCGF	4.12	8.13E-09	1.13E-05	1.20	7.46 19q13.3
26	231736_x_at	MGST1	3.57	7.41E-09	1.09E-05	1.19	7.44 12p12.3-p12.1
27	207961_x_at	MYH11	15.00	1.40E-07	6.63E-05	1.43	7.42 16p13.13-p13.12
28	224441_s_at	MGC14793	-3.13	8.20E-08	5.04E-05	-1.24	-7.37 6q16.3
29	205076_s_at	CRA	4.21	4.89E-08	3.77E-05	1.24	7.34 1q12-q21
30	210997_at	HGF	17.75	1.55E-07	6.94E-05	1.38	7.34 7q21.1
31	209975_at	CYP2E1	3.46	4.33E-08	3.47E-05	1.22	7.30 10q24.3-qter
32	224918_x_at	MGST1	3.27	1.58E-08	1.90E-05	1.18	7.29 12p12.3-p12.1
33	201069_at	MMP2	2.83	1.26E-08	1.59E-05	1.17	7.28 16q13-q21
34	202828_s_at	MMP14	5.47	1.26E-07	6.34E-05	1.29	7.25 14q11-q12
35	211709_s_at	SCGF	3.22	3.48E-08	3.08E-05	1.18	7.24 19q13.3
36	202283_at	SERPINF1	4.68	3.61E-08	3.08E-05	1.18	7.18 17p13.1
37	200852_x_at	GNB2	2.10	2.31E-08	2.65E-05	1.15	7.16 7q22
38	201688_s_at	TPD52	-3.31	7.77E-07	2.23E-04	-1.30	-7.14 8q21
39	219308_s_at	AK5	5.75	2.20E-07	9.06E-05	1.32	7.14 1p31
40	239814_at		2.34	2.50E-08	2.75E-05	1.14	7.12
41	200985_s_at	CD59	-6.95	2.61E-06	5.15E-04	-1.42	-7.09 11p13
42	242621_at	FLJ32468	1.47	2.87E-08	2.81E-05	1.14	7.08 7q22.1
43	202185_at	PLOD3	1.78	2.78E-08	2.81E-05	1.14	7.07 7q22
44	223136_at	AIG-1	-5.06	9.07E-07	2.45E-04	-1.28	-7.05 6q24.1
45	223091_x_at	GL004	-1.53	1.27E-07	6.34E-05	-1.17	-7.04 2q36.3
46	223354_x_at	GL004	-1.62	2.88E-07	1.09E-04	-1.21	-7.04 2q36.3
47	214797_s_at	PCTK3	-2.39	4.15E-07	1.44E-04	-1.22	-7.03 1q31-q32
48	214558_at	GPR12	1.53	4.99E-08	3.77E-05	1.14	7.01 13q12
49	229309_at		4.49	6.27E-08	4.25E-05	1.15	7.01
50	205859_at	LY86	3.30	2.78E-08	2.81E-05	1.12	7.01 6p24.3

2.7 inv(16) versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	-17.28	4.68E-43	1.11E-38	-1.58	-19.65	7p15-p14
2	235753_at		-9.51	1.52E-37	1.81E-33	-1.46	-17.75	
3	202370_s_at	CBFB	-2.85	2.71E-34	1.74E-30	-1.34	-16.58	16q22.1
4	209905_at	HOXA9	-49.46	2.93E-34	1.74E-30	-1.38	-16.55	7p15-p14
5	225055_at	DKFZp667M2411	-4.74	9.40E-32	3.72E-28	-1.31	-16.01	17q11.2
6	206847_s_at	HOXA7	-5.34	1.82E-33	8.62E-30	-1.26	-15.70	7p15-p14
7	227567_at		-4.87	2.00E-31	6.78E-28	-1.28	-15.69	
8	213150_at	HOXA10	-8.11	2.51E-31	7.45E-28	-1.19	-14.82	7p15-p14
9	213737_x_at		-2.49	2.13E-30	5.62E-27	-1.18	-14.69	
10	213147_at	HOXA10	-4.48	8.29E-26	8.20E-23	-1.20	-14.29	7p15-p14
11	235521_at	HOXA3	-15.59	1.02E-28	2.20E-25	-1.17	-14.19	7p15-p14
12	226352_at		-5.92	1.71E-29	4.05E-26	-1.13	-14.10	
13	209406_at	BAG2	-4.42	1.16E-28	2.30E-25	-1.11	-13.82	6p12.3-p11.2
14	213353_at	ABCA5	-3.50	6.04E-22	2.87E-19	-1.17	-13.54	17q24.3
15	205600_x_at	HOXB5	-2.61	7.86E-27	1.11E-23	-1.09	-13.48	17q21.3
16	232636_at	DKFZp547M2010	-10.69	7.96E-27	1.11E-23	-1.11	-13.44	Xq27.3
17	222786_at	C4S-2	-3.61	2.21E-27	4.04E-24	-1.07	-13.31	7p22
18	217963_s_at	NGFRAP1	-11.73	3.36E-27	5.70E-24	-1.06	-13.24	Xq22.1
19	201432_at	CAT	-2.19	7.17E-20	2.58E-17	-1.17	-13.16	11p13
20	219304_s_at	SCDGF-B	-3.85	7.59E-27	1.11E-23	-1.06	-13.15	11q22.3
21	213844_at	HOXA5	-8.27	3.64E-26	3.92E-23	-1.05	-13.03	7p15-p14
22	223044_at	SLC11A3	-9.45	1.35E-26	1.78E-23	-1.04	-13.02	2q32
23	223471_at	RAB3IP	-3.39	5.51E-25	4.51E-22	-1.06	-12.99	
24	219218_at	FLJ23058	-6.85	2.81E-26	3.17E-23	-1.04	-12.97	17q25.3
25	211031_s_at	CYLN2	-5.90	2.18E-26	2.73E-23	-1.04	-12.95	7q11.23
26	227224_at	FLJ25604	-5.22	1.47E-25	1.40E-22	-1.05	-12.93	1q24.2
27	230894_s_at		-11.16	2.66E-26	3.16E-23	-1.03	-12.91	
28	213908_at		-5.06	5.26E-26	5.42E-23	-1.04	-12.89	
29	233467_s_at	PHEMX	-1.84	1.87E-22	1.08E-19	-1.09	-12.89	11p15.5
30	229194_at		-2.74	1.68E-21	7.27E-19	-1.08	-12.73	
31	205366_s_at	HOXB6	-15.94	8.94E-25	6.85E-22	-1.05	-12.68	17q21.3
32	239791_at		-20.64	1.19E-24	8.86E-22	-1.06	-12.67	
33	235749_at	UGCGL2	-6.39	2.73E-25	2.49E-22	-1.00	-12.54	13q32.1
34	224952_at	DKFZP564D166	-3.67	1.66E-20	6.80E-18	-1.08	-12.51	17q23.3
35	225102_at	LOC152009	-4.87	4.14E-25	3.64E-22	-1.00	-12.50	3q21.3
36	236892_s_at		-16.62	4.37E-24	3.14E-21	-1.05	-12.46	
37	205601_s_at	HOXB5	-3.18	5.93E-25	4.69E-22	-1.00	-12.45	17q21.3
38	241706_at	LOC144402	-6.05	5.40E-25	4.51E-22	-1.00	-12.44	12q11
39	218414_s_at	NUDE1	-2.08	1.24E-23	8.66E-21	-1.01	-12.43	16p13.11
40	218477_at	PTD011	-2.94	1.42E-22	8.62E-20	-0.99	-12.08	6p12.1
41	201669_s_at	MARCKS	-12.15	1.50E-23	1.02E-20	-0.98	-12.08	6q22.2
42	235391_at	LOC137392	-9.70	2.13E-23	1.41E-20	-0.98	-12.04	8q21.3
43	200675_at	CD81	-3.09	1.41E-18	4.09E-16	-1.05	-12.00	11p15.5
44	231310_at		3.38	9.97E-13	1.11E-10	1.42	11.97	
45	213779_at	LOC129080	-2.87	2.71E-22	1.42E-19	-0.98	-11.93	22q12.1

#	affy id	HUGO name	fc	p	q	stn		Map Location
46	203949_at	MPO	2.10	4.63E-20	1.72E-17	1.01	11.91	17q23.1
47	228904_at		-5.66	3.84E-23	2.47E-20	-0.97	-11.89	
48	241985_at	FLJ37870	-6.15	5.95E-23	3.72E-20	-0.94	-11.70	5q13.3
49	200665_s_at	SPARC	5.30	4.17E-12	4.17E-10	1.45	11.63	5q31.3-q32
50	200984_s_at	CD59	-3.57	1.83E-22	1.08E-19	-0.93	-11.54	11p13

2.8   inv(16) versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	12.88	7.26E-18	1.92E-13	3.35	20.08	6p21.3
2	214450_at	CTSW	-8.03	6.77E-13	7.14E-10	-3.05	-15.96	11q13.1
3	38487_at	STAB1	-8.03	2.37E-12	1.95E-09	-3.01	-15.25	3p21.31
4	221004_s_at	ITM2C	-5.22	1.41E-13	3.01E-10	-2.58	-15.04	2q37
5	204661_at	CDW52	33.75	1.67E-13	3.15E-10	2.69	14.74	1p36
6	200654_at	P4HB	-2.30	1.92E-15	1.27E-11	-2.31	-14.63	17q25
7	203535_at	S100A9	9.01	7.53E-16	6.62E-12	2.24	14.32	1q21
8	217478_s_at	HLA-DMA	7.63	2.80E-14	8.72E-11	2.35	14.21	6p21.3
9	209732_at	CLECSF2	30.47	5.76E-13	6.61E-10	2.71	14.20	12p13-p12
10	34210_at	CDW52	43.85	7.27E-13	7.14E-10	2.58	13.90	1p36
11	238022_at		-8.74	2.99E-12	2.25E-09	-2.41	-13.63	
12	209619_at	CD74	5.65	3.24E-16	4.28E-12	2.06	13.52	5q32
13	201923_at	PRDX4	7.22	7.48E-14	1.79E-10	2.16	13.28	Xp22.13
14	205624_at	CPA3	-9.54	1.00E-11	6.01E-09	-2.41	-13.24	3q21-q25
15	204563_at	SELL	9.35	7.30E-13	7.14E-10	2.25	13.07	1q23-q25
16	200931_s_at	VCL	3.96	1.06E-14	5.62E-11	2.01	12.90	10q22.1-q23
17	231310_at		4.74	2.97E-14	8.72E-11	2.04	12.89	
18	209312_x_at	HLA-DRB1	8.89	3.15E-13	4.37E-10	2.06	12.62	6p21.3
19	208306_x_at	HLA-DRB4	9.65	5.23E-13	6.43E-10	2.08	12.60	6p21.3
20	238365_s_at		-10.74	1.01E-10	3.36E-08	-2.50	-12.45	
21	208891_at	DUSP6	7.70	2.11E-14	8.72E-11	1.93	12.44	12q22-q23
22	212953_x_at	CALR	-2.84	2.97E-14	8.72E-11	-1.91	-12.34	19p13.3-p13.2
23	204670_x_at	HLA-DRB5	6.79	3.94E-14	1.04E-10	1.91	12.25	6p21.3
24	205718_at	ITGB7	6.61	6.63E-13	7.14E-10	1.97	12.10	12q13.13
25	205453_at	HOXB2	11.16	1.03E-11	6.03E-09	2.13	11.95	17q21-q22
26	205663_at	PCBP3	-4.69	1.37E-11	7.52E-09	-2.01	-11.85	21q22.3
27	232617_at	CTSS	8.88	1.90E-11	9.29E-09	2.15	11.78	1q21
28	207375_s_at	IL15RA	4.80	1.48E-13	3.01E-10	1.84	11.77	10p15-p14
29	224583_at	COTL1	5.58	3.11E-13	4.37E-10	1.86	11.77	16q23.3
30	221059_s_at	CHST6	6.80	4.13E-12	2.80E-09	1.95	11.67	16q22
31	233072_at	KIAA1857	-7.47	2.04E-10	5.49E-08	-2.19	-11.60	9q34
32	229168_at	DKFZp434K0621	-6.73	3.74E-10	8.88E-08	-2.36	-11.59	5q35.3
33	208982_at	PECAM1	4.84	2.17E-12	1.85E-09	1.88	11.55	17q23

34	224839_s_at	GPT2	-9.02	4.23E-11	1.75E-08	-1.95	-11.41	16q12.1
35	202803_s_at	ITGB2	5.43	5.36E-13	6.43E-10	1.72	11.07	21q22.3
36	223280_x_at	MS4A6A	24.98	9.94E-11	3.36E-08	2.11	11.04	11q12.1
37	201496_x_at	MYH11	10.61	1.13E-11	6.47E-09	1.81	10.98	16p13.13-p13.12
38	211991_s_at	HLA-DPA1	25.17	9.82E-11	3.36E-08	2.05	10.97	6p21.3
39	204150_at	STAB1	-9.71	1.08E-09	2.11E-07	-2.26	-10.94	3p21.31
40	208689_s_at	RPN2	-1.75	1.91E-13	3.36E-10	-1.66	-10.90	20q12-q13.1
41	220798_x_at	FLJ11535	-3.81	7.69E-11	2.82E-08	-1.84	-10.89	19p13.3
42	201497_x_at	MYH11	28.44	1.48E-10	4.48E-08	2.16	10.88	16p13.13-p13.12
43	202917_s_at	S100A8	3.19	3.79E-13	5.01E-10	1.66	10.85	1q21
44	241742_at	PRAM-1	11.60	1.23E-10	3.81E-08	1.97	10.76	19p13.2
45	228046_at	LOC152485	3.03	5.49E-12	3.54E-09	1.72	10.76	4q31.1
46	226878_at		4.19	1.90E-11	9.29E-09	1.77	10.75	
47	238604_at		3.63	2.30E-13	3.79E-10	1.62	10.71	
48	213779_at	LOC129080	-6.64	9.66E-10	1.96E-07	-2.04	-10.68	22q12.1
49	224356_x_at	MS4A6A	25.23	2.22E-10	5.74E-08	2.06	10.62	11q12.1
50	217897_at	FXYD6	3.03	3.34E-11	1.44E-08	1.77	10.62	11q23.3

2.9   inv(16) versus t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	207075_at	CIAS1	6.59	1.58E-12	1.75E-08	2.20	12.68	1q44
2	208890_s_at	PLXNB2	5.12	3.17E-13	7.15E-09	1.97	12.18	22q13.33
3	205453_at	HOXB2	12.87	7.80E-12	3.24E-08	2.16	12.11	17q21-q22
4	205419_at	EBI2	7.52	3.29E-12	2.73E-08	2.01	11.90	13q32.2
5	205718_at	ITGB7	6.71	4.31E-13	7.15E-09	1.91	11.89	12q13.13
6	224764_at	ARHGAP10	8.78	1.26E-11	4.63E-08	2.02	11.59	10
7	201497_x_at	MYH11	26.12	1.56E-10	2.16E-07	2.14	10.85	16p13.13-p13.12
8	201496_x_at	MYH11	9.21	1.72E-11	5.70E-08	1.80	10.83	16p13.13-p13.12
9	224049_at	KCNK17	4.64	1.11E-10	1.77E-07	1.92	10.69	6p21.1
10	200665_s_at	SPARC	4.28	7.71E-12	3.24E-08	1.63	10.32	5q31.3-q32
11	224724_at	SULF2	26.61	4.15E-10	4.05E-07	1.99	10.28	20q12-13.2
12	218236_s_at	PRKCN	4.73	5.10E-12	3.10E-08	1.59	10.16	2p21
13	218795_at	ACP6	-4.42	3.10E-10	3.26E-07	-1.68	-10.03	1q21
14	201425_at	ALDH2	7.98	2.08E-10	2.50E-07	1.72	10.03	12q24.2
15	201944_at	HEXB	2.26	4.28E-11	1.01E-07	1.57	9.82	5q13
16	201887_at	IL13RA1	4.99	3.14E-10	3.26E-07	1.63	9.67	Xq24
17	201360_at	CST3	5.36	1.21E-10	1.83E-07	1.57	9.65	20p11.21
18	238604_at		3.10	5.61E-12	3.10E-08	1.46	9.56	
19	209365_s_at	ECM1	3.14	3.60E-11	9.96E-08	1.49	9.52	1q21
20	201596_x_at	KRT18	7.58	2.11E-10	2.50E-07	1.56	9.52	12q13
21	202670_at	MAP2K1	3.60	5.03E-10	4.58E-07	1.59	9.45	15q22.1-

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
								q22.33
22	203320_at	LNK	3.09	1.34E-10	1.94E-07	1.50	9.37	12q24
23	210314_x_at	TNFSF13	4.88	2.77E-10	3.06E-07	1.53	9.36	17p13.1
24	209500_x_at	TNFSF13	4.05	4.42E-10	4.19E-07	1.55	9.34	17p13.1
25	221841_s_at		4.04	3.60E-11	9.96E-08	1.42	9.21	
26	235359_at		2.91	1.88E-10	2.49E-07	1.47	9.20	
27	223249_at	CLDN12	3.53	1.06E-10	1.77E-07	1.44	9.16	7q21
28	218217_at	RISC	3.35	1.12E-10	1.77E-07	1.43	9.10	17q23.1
29	201739_at	SGK	4.42	4.17E-11	1.01E-07	1.40	9.07	6q23
30	229309_at		11.50	3.64E-09	1.89E-06	1.64	9.01	
31	240572_s_at		3.26	9.26E-11	1.77E-07	1.39	8.95	
32	208683_at	CAPN2	3.21	9.71E-11	1.77E-07	1.38	8.92	1q41-q42
33	225602_at	C9orf19	2.86	5.10E-11	1.13E-07	1.36	8.90	9p13-p12
34	226818_at	LOC219972	11.01	2.61E-09	1.63E-06	1.54	8.89	11q12.1
35	220974_x_at	BA108L7.2	4.78	3.85E-10	3.87E-07	1.39	8.79	10q24.31
36	229383_at		5.01	3.55E-09	1.87E-06	1.52	8.77	
37	212459_x_at	SUCLG2	3.54	8.98E-11	1.77E-07	1.34	8.72	3p14.2
38	205859_at	LY86	3.60	1.34E-09	1.01E-06	1.43	8.71	6p24.3
39	211084_x_at	PRKCN	4.82	2.26E-10	2.58E-07	1.33	8.60	2p21
40	236738_at		6.52	1.66E-09	1.20E-06	1.40	8.60	
41	217849_s_at	CDC42BPB	4.85	2.02E-10	2.50E-07	1.32	8.59	14q32.3
42	205330_at	MN1	9.06	1.06E-08	4.35E-06	1.56	8.52	22q12.1
43	204057_at	ICSBP1	4.27	5.50E-09	2.68E-06	1.44	8.46	16q24.1
44	228415_at	AP1S2	2.82	2.29E-09	1.52E-06	1.33	8.30	Xp22.31
45	202283_at	SERPINF1	8.45	2.79E-09	1.65E-06	1.34	8.29	17p13.1
46	226841_at	LOC219972	12.54	1.86E-08	6.29E-06	1.51	8.26	11q12.1
47	226137_at		3.27	4.82E-09	2.42E-06	1.36	8.26	
48	208033_s_at	ATBF1	3.76	1.34E-09	1.01E-06	1.30	8.24	16q22.3-q23.1
49	233555_s_at	SULF2	17.48	2.64E-08	8.12E-06	1.58	8.19	20q12-13.2
50	205076_s_at	CRA	5.49	1.56E-08	5.96E-06	1.44	8.19	1q12-q21

2.10 inv(3) versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205382_s_at	DF	-5.23	7.94E-22	5.04E-18	-1.05	-12.36	19p13.3
2	236892_s_at		-12.75	1.92E-23	4.88E-19	-1.02	-12.16	
3	239791_at		-11.42	4.78E-23	6.07E-19	-0.99	-11.89	
4	213844_at	HOXA5	-6.53	5.98E-20	2.53E-16	-1.01	-11.81	7p15-p14
5	213110_s_at	COL4A5	-16.77	4.56E-22	3.85E-18	-0.98	-11.63	Xq22
6	204082_at	PBX3	-4.66	3.88E-21	1.97E-17	-0.97	-11.52	9q33-q34
7	230480_at	HIWI2	-3.42	1.85E-19	6.72E-16	-0.92	-10.96	11q21
8	228904_at		-5.19	2.38E-19	7.54E-16	-0.89	-10.67	
9	204301_at	KIAA0711	-4.92	4.74E-19	1.34E-15	-0.89	-10.63	8p23.2
10	219304_s_at	SCDGF-B	-3.13	1.23E-16	2.60E-13	-0.89	-10.33	11q22.3
11	230743_at		-2.36	2.58E-17	5.95E-14	-0.88	-10.31	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
12	205767_at	EREG	-8.84	2.69E-18	6.83E-15	-0.83	-10.03	4q21.1
13	213893_x_at	PMS2L5	-1.96	9.34E-11	4.65E-08	-1.02	-9.84	7q11-q22
14	235753_at		-3.36	5.47E-13	5.78E-10	-0.91	-9.81	
15	226789_at		-2.42	2.56E-13	3.24E-10	-0.90	-9.77	
16	241464_s_at		-2.58	2.70E-15	4.89E-12	-0.84	-9.66	
17	226556_at		-2.94	1.47E-12	1.29E-09	-0.90	-9.59	
18	205600_x_at	HOXB5	-2.09	5.29E-13	5.78E-10	-0.88	-9.55	17q21.3
19	212318_at	TRN-SR	-2.02	1.62E-10	6.76E-08	-0.97	-9.47	7q32.2
20	204548_at	STAR	-4.50	5.21E-15	8.82E-12	-0.80	-9.36	8p11.2
21	204647_at	HOMER3	-4.86	2.10E-16	4.10E-13	-0.77	-9.35	19p13.11
22	240151_at		-2.60	1.42E-11	9.03E-09	-0.88	-9.25	
23	231300_at	LOC90835	-2.58	7.77E-12	5.48E-09	-0.86	-9.19	16p11.2
24	209905_at	HOXA9	-4.19	8.92E-12	5.96E-09	-0.83	-8.97	7p15-p14
25	223703_at	CDA017	-2.44	3.19E-13	3.85E-10	-0.79	-8.94	10q23.1
26	217499_x_at		-1.62	2.41E-13	3.24E-10	-0.78	-8.89	
27	212953_x_at	CALR	-1.58	4.78E-11	2.58E-08	-0.82	-8.71	19p13.3-p13.2
28	236398_s_at		-3.64	6.70E-11	3.54E-08	-0.82	-8.64	
29	210006_at	DKFZP564O243	-1.73	1.60E-11	9.88E-09	-0.78	-8.56	3p21.1
30	205624_at	CPA3	-6.67	1.90E-14	3.02E-11	-0.70	-8.52	3q21-q25
31	203746_s_at	HCCS	-1.55	4.25E-14	6.35E-11	-0.71	-8.49	Xp22.3
32	201186_at	LRPAP1	-2.64	2.54E-13	3.24E-10	-0.72	-8.45	4p16.3
33	213292_s_at	SNX13	-1.77	7.96E-10	2.43E-07	-0.82	-8.30	7p21.1
34	231175_at	FLJ30162	-6.23	9.91E-13	9.32E-10	-0.70	-8.20	6p11.1
35	212820_at	RC3	-2.87	1.13E-12	1.02E-09	-0.70	-8.16	15q15.3
36	235749_at	UGCGL2	-4.07	3.32E-10	1.19E-07	-0.77	-8.15	13q32.1
37	226123_at	LOC286180	-2.94	1.43E-10	6.17E-08	-0.76	-8.14	8q12.1
38	232250_at	KIAA1257	-3.37	9.87E-13	9.32E-10	-0.69	-8.14	3q21.3
39	214651_s_at	HOXA9	-3.07	6.40E-09	1.42E-06	-0.85	-8.12	7p15-p14
40	200700_s_at	KDELR2	-1.99	3.41E-10	1.20E-07	-0.77	-8.10	7p22.2
41	210115_at	RPL39L	-3.91	3.47E-13	4.00E-10	-0.66	-8.01	3q27
42	239503_at		-4.36	7.38E-13	7.50E-10	-0.66	-7.96	
43	208967_s_at	AK2	-2.18	5.27E-12	3.93E-09	-0.68	-7.94	1p34
44	205601_s_at	HOXB5	-2.53	1.16E-09	3.39E-07	-0.76	-7.93	17q21.3
45	203675_at	NUCB2	-2.09	7.25E-09	1.55E-06	-0.81	-7.92	11p15.1-p14
46	213150_at	HOXA10	-2.71	4.92E-10	1.62E-07	-0.73	-7.81	7p15-p14
47	242621_at	FLJ32468	-1.39	2.43E-10	9.34E-08	-0.71	-7.76	7q22.1
48	219551_at	TRAITS	-2.31	1.21E-10	5.72E-08	-0.70	-7.76	3q13.33
49	231736_x_at	MGST1	-3.01	1.93E-08	3.30E-06	-0.81	-7.75	12p12.3-p12.1
50	214575_s_at	AZU1	-4.54	2.96E-11	1.71E-08	-0.67	-7.73	19p13.3

2.11 inv(3) versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	212953_x_at	CALR		-5.95	2.17E-14	5.07E-11	-3.69	-18.88	19p13.3-p13.2

2	205382_s_at	DF	-12.24	2.37E-15	7.12E-12	-3.43	-18.68	19p13.3
3	203948_s_at	MPO	-9.29	4.98E-19	1.05E-14	-3.14	-18.57	17q23.1
4	203949_at	MPO	-6.22	1.52E-17	1.60E-13	-3.05	-17.82	17q23.1
5	200654_at	P4HB	-3.78	4.67E-17	3.27E-13	-2.71	-16.03	17q25
6	214450_at	CTSW	-8.62	1.58E-13	2.89E-10	-2.90	-15.67	11q13.1
7	231736_x_at	MGST1	-6.90	6.57E-16	2.30E-12	-2.57	-15.09	12p12.3-p12.1
8	224918_x_at	MGST1	-6.02	2.58E-16	1.15E-12	-2.54	-15.02	12p12.3-p12.1
9	206871_at	ELA2	-6.28	2.73E-16	1.15E-12	-2.54	-15.00	19p13.3
10	214575_s_at	AZU1	-12.19	2.49E-13	3.73E-10	-2.58	-14.34	19p13.3
11	205624_at	CPA3	-21.54	5.79E-12	5.79E-09	-2.85	-14.33	3q21-q25
12	208689_s_at	RPN2	-2.77	3.65E-15	9.58E-12	-2.43	-14.27	20q12-q13.1
13	238022_at		-8.14	1.08E-12	1.33E-09	-2.28	-12.89	
14	38487_at	STAB1	-5.21	5.94E-13	8.31E-10	-2.23	-12.76	3p21.31
15	221004_s_at	ITM2C	-4.36	8.93E-14	1.88E-10	-2.12	-12.49	2q37
16	217716_s_at	SEC61A1	-2.51	1.65E-13	2.89E-10	-2.09	-12.25	3q21.3
17	221739_at	IL27w	-2.24	2.31E-13	3.73E-10	-2.06	-12.11	19p13.3
18	233072_at	KIAA1857	-10.04	1.05E-10	5.14E-08	-2.37	-12.06	9q34
19	208852_s_at	CANX	-2.94	3.24E-12	3.78E-09	-2.07	-11.86	5q35
20	220798_x_at	FLJ11535	-5.26	7.78E-12	6.81E-09	-2.05	-11.62	19p13.3
21	217225_x_at	LOC283820	-2.41	9.52E-13	1.25E-09	-1.94	-11.43	16p13.13
22	208730_x_at	RAB2	2.53	8.63E-10	3.12E-07	2.18	11.42	8q12.1
23	203675_at	NUCB2	-3.92	6.96E-12	6.65E-09	-2.00	-11.42	11p15.1-p14
24	201004_at	SSR4	-2.77	1.64E-11	1.15E-08	-2.00	-11.33	Xq28
25	210788_s_at	retSDR4	-2.65	7.69E-12	6.81E-09	-1.95	-11.22	14q22.3
26	202759_s_at	AKAP2	-4.78	2.58E-11	1.69E-08	-1.98	-11.15	9q31-q33
27	209619_at	CD74	4.57	1.47E-11	1.14E-08	1.92	11.07	5q32
28	214315_x_at	CALR	-3.14	2.25E-11	1.52E-08	-1.93	-11.00	19p13.3-p13.2
29	229168_at	DKFZp434K0621	-5.62	4.18E-10	1.72E-07	-2.12	-10.99	5q35.3
30	211990_at	HLA-DPA1	12.02	1.70E-08	3.31E-06	2.38	10.92	6p21.3
31	214797_s_at	PCTK3	6.22	2.95E-09	8.48E-07	2.12	10.91	1q31-q32
32	211709_s_at	SCGF	-5.08	3.77E-12	3.96E-09	-1.80	-10.65	19q13.3
33	200068_s_at - HG-U133A	CANX	-1.76	3.59E-12	3.96E-09	-1.79	-10.61	5q35
34	206914_at	CRTAM	6.82	3.01E-09	8.54E-07	1.99	10.50	11q22-q23
35	204897_at	PTGER4	5.48	3.25E-10	1.37E-07	1.87	10.44	5p13.1
36	221253_s_at	MGC3178	-3.45	5.95E-11	3.62E-08	-1.81	-10.36	6p24.3
37	225010_at	D10S170	2.56	2.69E-11	1.71E-08	1.77	10.33	10q21
38	210140_at	CST7	-8.79	1.17E-09	4.09E-07	-1.98	-10.32	20p11.21
39	226905_at		-1.96	8.40E-11	4.20E-08	-1.78	-10.24	
40	200652_at	SSR2	-1.91	1.02E-11	8.61E-09	-1.73	-10.22	1q21-q23
41	33323_r_at	SFN	1.93	1.07E-11	8.68E-09	1.73	10.21	1p35.3
42	227353_at	EVER2	5.28	1.34E-08	2.75E-06	2.02	10.17	17q25.3
43	224839_s_at	GPT2	-6.13	8.34E-11	4.20E-08	-1.77	-10.15	16q12.1
44	200068_s_at - HG-U133B	CANX	-1.67	1.62E-11	1.15E-08	-1.72	-10.14	5q35

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
45 209215_at		TETRAN	-3.38	1.52E-11	1.14E-08	-1.72	-10.14	4p16.3
46 205614_x_at		MST1	-8.62	3.49E-09	9.53E-07	-2.00	-9.99	3p21
47 241383_at			-4.56	2.13E-09	6.47E-07	-1.87	-9.85	
48 214317_x_at		RPS9	2.30	1.38E-09	4.55E-07	1.77	9.82	19q13.4
49 202487_s_at		H2AV	-2.25	6.02E-11	3.62E-08	-1.64	-9.66	7p13
50 204661_at		CDW52	22.88	1.06E-07	1.35E-05	2.16	9.63	1p36

2.12 inv(3) versus t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1 203949_at		MPO	-5.73	1.58E-13	3.73E-09	-2.14	-12.41	17q23.1
2 211084_x_at		PRKCN	6.08	3.25E-10	1.92E-06	1.92	10.59	2p21
3 225010_at		D10S170	2.96	1.16E-11	1.38E-07	1.78	10.37	10q21
4 233955_x_at		HSPC195	5.19	3.37E-08	8.86E-05	2.18	10.19	5q31.3
5 203948_s_at		MPO	-6.82	1.36E-10	1.07E-06	-1.74	-9.93	17q23.1
6 217963_s_at		NGFRAP1	29.01	4.74E-07	3.74E-04	2.04	8.67	Xq22.1
7 224516_s_at		HSPC195	5.87	5.57E-07	3.79E-04	1.92	8.45	5q31.3
8 219478_at		WFDC1	-12.35	6.15E-08	1.28E-04	-1.68	-8.45	16q24.3
9 217226_s_at		BA108L7.2	3.53	7.38E-08	1.28E-04	1.58	8.38	10q24.31
10 231180_at			-2.35	2.92E-09	1.38E-05	-1.42	-8.23	
11 201281_at		ADRM1	-2.17	1.21E-08	4.62E-05	-1.45	-8.15	20q13.33
12 212423_at		FLJ90798	4.18	7.41E-08	1.28E-04	1.49	8.07	10q22.3
13 222996_s_at		HSPC195	4.31	1.08E-06	4.79E-04	1.79	7.98	5q31.3
14 228827_at			-95.46	2.85E-07	2.93E-04	-1.78	-7.91	
15 230259_at			-1.91	2.21E-08	6.52E-05	-1.37	-7.77	
16 213716_s_at		SECTM1	5.01	2.54E-07	2.86E-04	1.44	7.68	17q25
17 211709_s_at		SCGF	-3.55	1.37E-08	4.62E-05	-1.30	-7.56	19q13.3
18 202759_s_at		AKAP2	-4.91	2.29E-07	2.71E-04	-1.45	-7.56	9q31-q33
19 219165_at		PDLIM2	3.79	6.33E-07	4.00E-04	1.48	7.55	8p21.2
20 206478_at		KIAA0125	23.32	2.67E-06	8.31E-04	1.89	7.54	14q32.33
21 205529_s_at		CBFA2T1	-13.48	6.51E-07	4.00E-04	-1.63	-7.44	8q22
22 212895_s_at		ABR	3.03	3.97E-07	3.50E-04	1.38	7.38	17p13.3
23 223534_s_at		RPS6KL1	-2.20	8.42E-08	1.33E-04	-1.31	-7.37	14q24.2
24 212953_x_at		CALR	-2.47	3.99E-07	3.50E-04	-1.42	-7.33	19p13.3-p13.2
25 206295_at		IL18	3.69	1.85E-06	6.95E-04	1.52	7.33	11q22.2-q22.3
26 202006_at		PTPN12	2.76	6.85E-07	4.00E-04	1.39	7.29	7q11.23
27 220974_x_at		BA108L7.2	4.34	5.65E-07	3.79E-04	1.37	7.27	10q24.31
28 201243_s_at		ATP1B1	5.21	2.00E-06	7.03E-04	1.50	7.27	1q22-q25
29 201938_at		CDK2AP1	2.10	7.57E-08	1.28E-04	1.27	7.26	12q24.31
30 207839_s_at		LOC51754	3.16	2.14E-07	2.66E-04	1.30	7.24	9p13.1
31 203820_s_at		KOC1	3.93	2.73E-06	8.37E-04	1.53	7.19	7p11
32 202887_s_at		RTP801	4.32	1.72E-06	6.79E-04	1.44	7.17	10pter-q26.12
33 215051_x_at		AIF1	2.69	1.90E-07	2.49E-04	1.28	7.17	6p21.3
34 214042_s_at		RPL22	1.48	7.74E-07	4.16E-04	1.35	7.15	1p36.3-p36.2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
35	227620_at		3.79	3.71E-07	3.50E-04	1.27	7.03	
36	210150_s_at	LAMA5	-4.17	5.29E-07	3.79E-04	-1.31	-7.01	20q13.2-q13.3
37	230659_at	KIAA0212	-2.09	5.37E-07	3.79E-04	-1.30	-6.99	3p26.1
38	221773_at		3.81	8.38E-07	4.31E-04	1.30	6.99	
39	226865_at		8.49	5.84E-06	1.21E-03	1.64	6.98	
40	242621_at	FLJ32468	-1.58	2.69E-07	2.90E-04	-1.24	-6.95	7q22.1
41	229406_at		-11.72	1.19E-06	4.98E-04	-1.39	-6.94	
42	214317_x_at	RPS9	2.15	7.51E-08	1.28E-04	1.19	6.93	19q13.4
43	213908_at		3.96	2.61E-06	8.24E-04	1.38	6.92	
44	204494_s_at	DKFZP434H132	4.90	6.20E-06	1.21E-03	1.56	6.89	15q22.33
45	214807_at		2.91	2.89E-06	8.66E-04	1.34	6.80	
46	220377_at	C14orf110	239.90	8.80E-06	1.40E-03	1.75	6.79	14q32.33
47	221458_at	HTR1F	2.55	2.14E-06	7.23E-04	1.30	6.77	3p12
48	227279_at	MGC15737	3.22	4.36E-06	1.08E-03	1.38	6.76	Xq22.1
49	206871_at	ELA2	-5.10	6.92E-07	4.00E-04	-1.22	-6.69	19p13.3
50	235199_at		2.76	1.11E-06	4.79E-04	1.22	6.68	

2.13 normal versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213147_at	HOXA10	17.20	7.61E-48	1.35E-43	1.80	21.98	7p15-p14
2	214651_s_at	HOXA9	165.25	6.03E-45	5.33E-41	1.86	21.56	7p15-p14
3	209732_at	CLECSF2	20.01	1.05E-43	6.19E-40	1.69	20.43	12p13-p12
4	217848_s_at	PP	4.53	1.30E-33	1.43E-30	1.63	19.10	10q11.1-q24
5	204425_at	ARHGAP4	16.00	7.32E-40	3.24E-36	1.51	18.45	Xq28
6	203948_s_at	MPO	-4.31	4.91E-18	4.88E-16	-1.99	-18.44	17q23.1
7	235753_at		11.39	2.85E-38	8.41E-35	1.52	18.22	
8	213587_s_at	LOC155066	5.69	1.56E-39	5.53E-36	1.47	18.14	7q36.1
9	205453_at	HOXB2	17.64	8.27E-37	1.83E-33	1.45	17.52	17q21-q22
10	213150_at	HOXA10	32.28	6.55E-36	1.16E-32	1.44	17.25	7p15-p14
11	205771_s_at	AKAP7	11.23	4.80E-37	1.21E-33	1.39	17.15	6q23
12	204563_at	SELL	6.36	1.44E-35	2.13E-32	1.39	17.03	1q23-q25
13	209905_at	HOXA9	427.11	6.92E-35	9.41E-32	1.48	16.97	7p15-p14
14	211990_at	HLA-DPA1	8.89	1.52E-36	2.99E-33	1.37	16.90	6p21.3
15	206847_s_at	HOXA7	7.10	8.12E-36	1.31E-32	1.37	16.80	7p15-p14
16	212953_x_at	CALR	-3.76	2.76E-13	1.05E-11	-2.63	-16.73	19p13.3-p13.2
17	201923_at	PRDX4	5.34	1.07E-29	8.98E-27	1.41	16.60	Xp22.13
18	203949_at	MPO	-2.75	3.27E-21	5.78E-19	-1.51	-16.17	17q23.1
19	213844_at	HOXA5	26.04	1.50E-33	1.56E-30	1.34	16.13	7p15-p14
20	241742_at	PRAM-1	6.31	4.59E-34	5.80E-31	1.30	15.99	19p13.2
21	204362_at	SCAP2	14.27	5.48E-34	6.46E-31	1.30	15.95	7p21-p15
22	221004_s_at	ITM2C	-6.45	8.06E-14	3.48E-12	-2.07	-15.90	2q37
23	228113_at	STAT3	4.35	9.90E-29	7.00E-26	1.33	15.79	17q21
24	236322_at		6.34	1.24E-29	9.99E-27	1.32	15.79	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
25	214797_s_at	PCTK3	4.80	5.08E-26	2.15E-23	1.33	15.44	1q31-q32
26	225639_at	SCAP2	11.62	1.80E-32	1.77E-29	1.25	15.40	7p21-p15
27	200654_at	P4HB	-2.36	1.03E-15	6.62E-14	-1.67	-15.39	17q25
28	214450_at	CTSW	-6.52	9.60E-13	3.22E-11	-2.30	-15.35	11q13.1
29	38487_at	STAB1	-7.03	1.98E-12	6.20E-11	-2.21	-14.76	3p21.31
30	235521_at	HOXA3	24.52	1.32E-29	1.02E-26	1.24	14.69	7p15-p14
31	231767_at	HOXB4	4.88	1.66E-30	1.54E-27	1.18	14.57	17q21-q22
32	200931_s_at	VCL	3.67	3.82E-27	2.01E-24	1.22	14.54	10q22.1-q23
33	238058_at		4.07	7.32E-30	6.47E-27	1.18	14.42	
34	205600_x_at	HOXB5	2.95	4.70E-28	2.97E-25	1.19	14.39	17q21.3
35	231832_at	GALNT4	3.19	6.19E-21	1.01E-18	1.29	14.33	12q21.3-q22
36	236554_x_at	EVER2	3.51	5.84E-24	1.75E-21	1.22	14.20	17q25.3
37	216899_s_at	SCAP2	6.57	1.91E-29	1.41E-26	1.15	14.17	7p21-p15
38	225314_at	MGC45416	2.69	2.33E-26	1.12E-23	1.16	13.93	4p11
39	207375_s_at	IL15RA	4.72	1.94E-26	9.54E-24	1.16	13.93	10p15-p14
40	227598_at	LOC113763	4.28	5.64E-28	3.44E-25	1.13	13.81	7q35
41	204361_s_at	SCAP2	9.69	3.06E-28	2.08E-25	1.12	13.77	7p21-p15
42	228904_at		13.76	3.02E-27	1.67E-24	1.16	13.73	
43	226106_at	ZFP26	4.85	3.68E-28	2.41E-25	1.11	13.73	11p15.3
44	227353_at	EVER2	3.42	1.63E-20	2.44E-18	1.23	13.71	17q25.3
45	222423_at	NDFIP1	3.39	2.13E-24	6.97E-22	1.16	13.70	5q31.3
46	213388_at		6.14	2.72E-26	1.27E-23	1.13	13.68	
47	227999_at	LOC170394	3.01	4.28E-21	7.50E-19	1.20	13.64	10q26.3
48	201753_s_at	ADD3	5.82	3.86E-27	2.01E-24	1.10	13.53	10q24.2-q24.3
49	201719_s_at	EPB41L2	10.16	1.49E-27	8.49E-25	1.10	13.52	6q23
50	210145_at	PLA2G4A	6.98	1.16E-27	6.86E-25	1.10	13.50	1q25

2.14 normal versus t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	145.42	6.40E-45	1.76E-40	1.85	21.54	7p15-p14
2	213147_at	HOXA10	11.17	2.55E-44	3.50E-40	1.64	20.18	7p15-p14
3	235753_at		10.27	6.99E-38	6.39E-34	1.48	17.88	
4	205453_at	HOXB2	20.36	3.89E-37	2.14E-33	1.47	17.66	17q21-q22
5	213150_at	HOXA10	39.50	3.93E-36	1.80E-32	1.46	17.37	7p15-p14
6	206847_s_at	HOXA7	6.33	3.12E-37	2.14E-33	1.40	17.21	7p15-p14
7	209905_at	HOXA9	373.92	7.12E-35	2.79E-31	1.47	16.97	7p15-p14
8	221581_s_at	WBSCR5	6.07	3.59E-33	1.23E-29	1.27	15.64	7q11.23
9	213844_at	HOXA5	14.53	3.73E-32	1.14E-28	1.26	15.37	7p15-p14
10	235521_at	HOXA3	19.62	3.18E-29	7.94E-26	1.23	14.53	7p15-p14
11	217963_s_at	NGFRAP1	16.68	2.36E-29	6.47E-26	1.17	14.24	Xq22.1
12	243806_at		4.41	5.47E-27	1.07E-23	1.12	13.65	
13	228904_at		13.05	4.26E-27	8.99E-24	1.15	13.65	

# affy id	HUGO name	fc	p	q	stn	t	Map Location	
14 225615_at	LOC126917	6.55	1.29E-27	2.95E-24	1.10	13.52	1p36.13	
15 233955_x_at	HSPC195	3.26	3.10E-26	5.32E-23	1.11	13.42	5q31.3	
16 227279_at	MGC15737	2.67	1.87E-20	1.20E-17	1.19	13.37	Xq22.1	
17 213908_at		5.06	1.20E-26	2.19E-23	1.08	13.21		
18 205366_s_at	HOXB6	33.49	6.39E-26	9.74E-23	1.13	13.21	17q21.3	
19 215087_at		3.73	3.61E-26	5.82E-23	1.05	12.95		
20 231767_at	HOXB4	3.96	2.89E-25	3.96E-22	1.06	12.93	17q21-q22	
21 241370_at		3.39	1.53E-25	2.21E-22	1.05	12.88		
22 236892_s_at		20.18	1.96E-24	2.44E-21	1.06	12.59		
23 228365_at	LOC144402	8.45	8.27E-25	1.08E-21	1.03	12.58	12q11	
24 203017_s_at	SSX2IP	3.94	6.95E-24	7.62E-21	1.03	12.52		
25 204069_at	MEIS1	13.42	4.38E-24	5.01E-21	1.04	12.43	2p14-p13	
26 205601_s_at	HOXB5	3.11	2.82E-24	3.36E-21	1.01	12.36	17q21.3	
27 239791_at		12.91	1.21E-23	1.28E-20	1.02	12.23		
28 206310_at	SPINK2	53.74	2.36E-23	2.23E-20	1.04	12.19	4q12	
29 238077_at	MGC27385	3.78	1.86E-23	1.82E-20	0.99	12.12	3p21.1	
30 208091_s_at	DKFZP564K0822	5.35	7.06E-23	5.70E-20	1.00	12.10	7p14.1	
31 226206_at	FLJ32205	2.54	1.36E-19	7.91E-17	1.04	12.05	7p22.3	
32 230894_s_at		7.46	1.35E-23	1.37E-20	0.98	12.03		
33 205600_x_at	HOXB5	2.56	8.19E-20	4.88E-17	1.04	12.02	17q21.3	
34 226865_at		6.47	3.94E-23	3.49E-20	0.98	11.92		
35 222996_s_at	HSPC195	2.52	5.88E-23	4.89E-20	0.98	11.92	5q31.3	
36 238756_at		4.33	4.37E-23	3.75E-20	0.97	11.90		
37 203680_at	PRKAR2B	6.19	3.16E-23	2.89E-20	0.97	11.86	7q22-q31.1	
38 241706_at	LOC144402	5.37	2.55E-22	1.95E-19	0.96	11.74	12q11	
39 204494_s_at	DKFZP434H132	2.88	4.33E-22	3.05E-19	0.95	11.60	15q22.33	
40 224516_s_at	HSPC195	3.18	1.86E-22	1.46E-19	0.94	11.59	5q31.3	
41 233467_s_at	PHEMX	2.18	4.65E-14	9.67E-12	1.14	11.58	11p15.5	
42 204495_s_at	DKFZP434H132	2.75	4.31E-22	3.05E-19	0.95	11.58	15q22.33	
43 238778_at	FLJ32798	9.22	4.01E-22	2.97E-19	0.94	11.48	10p11.1	
44 227853_at		3.12	1.50E-17	6.34E-15	1.01	11.47		
45 202006_at	PTPN12	2.49	6.57E-17	2.50E-14	1.00	11.26	7q11.23	
46 226134_s_at		5.05	1.67E-21	1.15E-18	0.91	11.20		
47 218772_x_at	FLJ10493	2.92	5.63E-17	2.18E-14	0.98	11.09	9q31.2	
48 238012_at		2.14	1.19E-16	4.14E-14	0.98	11.04		
49 238455_at		4.27	4.48E-21	3.00E-18	0.90	11.04		
50 224764_at	ARHGAP10	4.58	1.17E-20	7.64E-18	0.90	11.01		10

2.15 t(15;17) versus t(8;21)

# affy id	HUGO name	fc	p	q	stn	t	Map Location
1 214450_at	CTSW	28.73	1.65E-13	4.59E-09	3.58	17.73	11q13.1
2 38487_at	STAB1	19.69	4.77E-13	4.59E-09	3.26	16.49	3p21.31
3 209732_at	CLECSF2	-30.76	2.95E-12	1.46E-08	-3.39	-16.10	12p13-p12
4 211990_at	HLA-DPA1	-10.92	1.76E-11	5.09E-08	-2.53	-13.40	6p21.3

5	224839_s_at	GPT2	12.98	6.62E-11	1.19E-07	2.37	12.32 16q12.1
6	212509_s_at		10.31	9.35E-11	1.59E-07	2.37	12.20
7	204150_at	STAB1	21.33	3.55E-10	4.10E-07	2.36	11.58 3p21.31
8	201596_x_at	KRT18	20.06	3.29E-10	3.96E-07	2.28	11.50 12q13
9	221004_s_at	ITM2C	3.37	4.65E-13	4.59E-09	1.86	11.42 2q37
10	205349_at	GNA15	3.53	3.47E-11	8.35E-08	2.00	11.42 19p13.3
11	205663_at	PCBP3	4.49	9.95E-12	3.59E-08	1.92	11.33 21q22.3
12	226878_at		-5.52	8.96E-10	7.61E-07	-2.06	-10.80
13	212953_x_at	CALR	2.41	1.19E-12	8.57E-09	1.74	10.78 19p13.3-p13.2
14	227326_at		5.43	2.89E-10	3.63E-07	1.89	10.58
15	217716_s_at	SEC61A1	2.09	3.73E-12	1.54E-08	1.70	10.48 3q21.3
16	228113_at	STAT3	-5.12	5.53E-10	5.50E-07	-1.86	-10.38 17q21
17	200986_at	SERPING1	9.81	1.47E-09	1.09E-06	1.98	10.34 11q12-q13.1
18	208689_s_at	RPN2	1.79	3.03E-12	1.46E-08	1.63	10.17 20q12-q13.1
19	217478_s_at	HLA-DMA	-5.35	6.89E-10	6.42E-07	-1.81	-10.15 6p21.3
20	204316_at	RGS10	-2.45	1.99E-10	2.67E-07	-1.73	-10.10 10q25
21	209021_x_at	KIAA0652	4.43	3.36E-11	8.35E-08	1.61	9.83 11p11.12
22	205614_x_at	MST1	7.54	3.75E-09	2.30E-06	1.83	9.69 3p21
23	209619_at	CD74	-4.60	1.28E-10	1.95E-07	-1.60	-9.66 5q32
24	200953_s_at	CCND2	2.70	4.02E-10	4.30E-07	1.65	9.66 12p13
25	208852_s_at	CANX	2.32	6.39E-11	1.19E-07	1.57	9.60 5q35
26	208826_x_at	HINT1	1.43	5.89E-11	1.19E-07	1.56	9.58 5q31.2
27	201522_x_at	SNRPN	-3.65	1.70E-11	5.09E-08	-1.53	-9.54 15q12
28	201136_at	PLP2	2.76	2.03E-10	2.67E-07	1.56	9.41 Xp11.23
29	201137_s_at	HLA-DPB1	-13.39	1.86E-08	7.79E-06	-1.93	-9.37 6p21.3
30	201425_at	ALDH2	5.16	1.10E-09	8.76E-07	1.61	9.35 12q24.2
31	204670_x_at	HLA-DRB5	-5.72	8.74E-10	7.61E-07	-1.58	-9.30 6p21.3
32	201952_at	ALCAM	4.64	2.50E-09	1.76E-06	1.65	9.30 3q13.1
33	211991_s_at	HLA-DPA1	-17.00	2.54E-08	9.11E-06	-1.85	-9.13 6p21.3
34	209312_x_at	HLA-DRB1	-6.80	5.84E-09	3.18E-06	-1.63	-9.09 6p21.3
35	238022_at		4.06	6.47E-11	1.19E-07	1.46	9.09
36	211474_s_at	SERPINB6	-5.69	1.90E-08	7.82E-06	-1.74	-9.06 6p25
37	223321_s_at	FGFRL1	3.74	4.94E-09	2.89E-06	1.61	9.02 4p16
38	201894_s_at	DCN	2.05	1.13E-10	1.81E-07	1.42	8.86 12q13.2
39	208885_at	LCP1	2.18	1.50E-10	2.16E-07	1.42	8.85 13q14.3
40	201923_at	PRDX4	-5.83	1.40E-08	6.42E-06	-1.61	-8.82 Xp22.13
41	209344_at	TPM4	6.87	2.27E-08	8.69E-06	1.69	8.80 19p13.1
42	227353_at	EVER2	-3.83	4.90E-09	2.89E-06	-1.52	-8.79 17q25.3
43	202732_at	PKIG	2.65	2.70E-09	1.79E-06	1.49	8.74 20q12-q13.1
44	208306_x_at	HLA-DRB4	-7.05	1.62E-08	7.08E-06	-1.57	-8.69 6p21.3
45	55093_at	CSGlcA-T	1.87	6.61E-10	6.36E-07	1.41	8.65 7q36.1
46	201360_at	CST3	4.20	2.73E-09	1.79E-06	1.45	8.61 20p11.21
47	221799_at	CSGlcA-T	2.51	3.90E-10	4.30E-07	1.38	8.59 7q36.1
48	201581_at	DJ971N18.2	2.54	2.69E-09	1.79E-06	1.44	8.58 20p12
49	207721_x_at	HINT1	1.55	5.39E-10	5.50E-07	1.38	8.52 5q31.2
50	205035_at	CTDP1	2.57	1.34E-08	6.42E-06	1.51	8.51 18q23

Table 3

3. One-Versus-All
(OVA)

3.1   11q23 versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202746_at	ITM2A	-12.91	2.85E-24	8.05E-20	-1.40	-14.06	Xq13.3-Xq21.2
2	202747_s_at	ITM2A	-12.74	3.31E-23	4.67E-19	-1.33	-13.40	Xq13.3-Xq21.2
3	200953_s_at	CCND2	-4.13	6.99E-23	6.58E-19	-1.21	-12.64	12p13
4	214651_s_at	HOXA9	16.91	7.73E-14	7.53E-11	1.76	12.47	7p15-p14
5	200951_s_at	CCND2	-4.70	1.60E-20	1.13E-16	-1.12	-11.63	12p13
6	201830_s_at	NET1	-3.86	5.10E-20	2.88E-16	-1.10	-11.41	10p15
7	225831_at	LOC148894	-3.63	1.18E-19	5.56E-16	-1.08	-11.20	1p36.11
8	206847_s_at	HOXA7	5.87	3.36E-12	1.73E-09	1.49	10.73	7p15-p14
9	213147_at	HOXA10	6.79	2.99E-12	1.65E-09	1.41	10.60	7p15-p14
10	235753_at		10.50	1.61E-11	6.13E-09	1.59	10.33	
11	201015_s_at	JUP	-5.70	3.82E-17	1.20E-13	-1.00	-10.30	17q21
12	225344_at	ERAP140	-3.86	7.59E-17	1.95E-13	-1.02	-10.29	6q22.33
13	201829_at	NET1	-2.51	1.29E-17	5.22E-14	-0.99	-10.28	10p15
14	200665_s_at	SPARC	-9.29	1.02E-16	2.40E-13	-1.01	-10.18	5q31.3-q32
15	235818_at		-8.40	5.28E-17	1.49E-13	-0.99	-10.15	
16	225653_at		-1.86	3.48E-17	1.20E-13	-0.97	-10.10	
17	214390_s_at	BCAT1	-8.46	1.87E-16	4.06E-13	-1.00	-10.07	12pter-q12
18	226517_at	BCAT1	-9.42	3.34E-16	6.75E-13	-1.02	-10.07	12pter-q12
19	213737_x_at		2.30	5.27E-13	3.72E-10	1.13	10.03	
20	204082_at	PBX3	6.73	7.32E-11	2.11E-08	1.46	9.67	9q33-q34
21	227297_at		-12.11	4.62E-15	6.87E-12	-0.99	-9.60	
22	206761_at	TACTILE	-14.31	6.00E-15	8.47E-12	-1.01	-9.60	3q13.13
23	209905_at	HOXA9	30.79	1.17E-10	3.18E-08	1.50	9.53	7p15-p14
24	206009_at	ITGA9	-2.94	1.25E-15	2.35E-12	-0.91	-9.45	3p21.3
25	231259_s_at	CCND2	-2.38	1.75E-15	3.09E-12	-0.91	-9.41	12p13
26	218966_at	MYO5C	-2.46	2.13E-15	3.54E-12	-0.89	-9.28	15q21
27	221581_s_at	WBSCR5	3.27	3.80E-11	1.28E-08	1.14	9.23	7q11.23
28	221235_s_at		-2.14	3.45E-15	5.41E-12	-0.88	-9.21	
29	216417_x_at	HOXB9	2.85	6.70E-11	1.99E-08	1.16	9.15	17q21.3
30	241756_at		-3.10	6.30E-15	8.47E-12	-0.87	-9.08	
31	218041_x_at	SLC38A2	-1.64	3.37E-12	1.73E-09	-0.97	-8.98	12q
32	242051_at		-2.87	1.05E-14	1.32E-11	-0.86	-8.98	
33	219188_s_at	LRP16	-2.96	1.08E-14	1.32E-11	-0.86	-8.98	11q11
34	212667_at	SPARC	-4.84	1.65E-14	1.95E-11	-0.86	-8.92	5q31.3-q32
35	220104_at	ZAP	-2.23	4.58E-14	4.98E-11	-0.86	-8.87	7q34
36	221831_at	LOC148894	-2.48	1.75E-13	1.54E-10	-0.87	-8.81	1p36.11
37	213908_at		7.26	6.80E-10	1.40E-07	1.30	8.75	
38	219686_at	HSA250839	-9.62	2.75E-13	2.10E-10	-0.92	-8.75	4p16.2
39	225285_at		-7.72	6.68E-14	7.00E-11	-0.85	-8.72	

# affy id	HUGO name	fc	p	q	stn	t	Map Location
40 200952_s_at	CCND2	-2.56	4.37E-14	4.94E-11	-0.83	-8.71	12p13
41 224049_at	KCNK17	-2.91	6.94E-14	7.00E-11	-0.84	-8.70	6p21.1
42 209679_s_at	LOC57228	-2.41	1.91E-13	1.54E-10	-0.84	-8.61	12q13.12
43 201029_s_at	CD99	-1.87	9.29E-12	3.92E-09	-0.91	-8.59	Xp22.32
44 218825_at	ZNEU1	-4.68	8.83E-14	8.32E-11	-0.82	-8.57	9q34.3
45 214439_x_at	BIN1	-2.63	1.56E-13	1.43E-10	-0.83	-8.55	2q14
46 213150_at	HOXA10	11.23	1.27E-09	2.33E-07	1.28	8.51	7p15-p14
47 228058_at	LOC124220	-4.30	7.66E-13	5.03E-10	-0.84	-8.50	16p13.3
48 201564_s_at	FSCN1	-4.90	1.88E-13	1.54E-10	-0.82	-8.49	7p22
49 200602_at	APP	-5.79	1.86E-13	1.54E-10	-0.81	-8.42	21q21.3
50 221832_s_at	LOC148894	-2.54	3.02E-13	2.24E-10	-0.81	-8.41	1p36.11

3.2 inv(16) versus rest

# affy id	HUGO name	fc	p	q	stn	t	Map Location
1 227567_at		-4.44	1.09E-23	3.61E-19	-1.25	-13.05	
2 225055_at	DKFZp667M2411	-4.65	8.12E-22	1.34E-17	-1.16	-12.13	17q11.2
3 224952_at	DKFZP564D166	-3.64	2.43E-19	2.01E-15	-1.18	-11.90	17q23.3
4 202370_s_at	CBFB	-2.54	2.73E-20	3.01E-16	-1.10	-11.45	16q22.1
5 201497_x_at	MYH11	24.43	1.67E-10	9.18E-08	2.11	10.82	16p13.13-p13.12
6 213737_x_at		-2.57	1.66E-18	1.09E-14	-1.04	-10.78	
7 201496_x_at	MYH11	6.76	9.51E-11	5.61E-08	1.66	10.72	16p13.13-p13.12
8 200675_at	CD81	-3.20	9.31E-18	4.39E-14	-1.04	-10.70	11p15.5
9 225102_at	LOC152009	-4.43	5.82E-18	3.20E-14	-1.00	-10.44	3q21.3
10 200665_s_at	SPARC	4.00	1.11E-11	1.00E-08	1.28	10.36	5q31.3-q32
11 223471_at	RAB3IP	-2.82	1.34E-16	5.54E-13	-0.96	-9.93	
12 228497_at	FLIPT1	-5.27	5.36E-16	1.97E-12	-0.97	-9.81	1p13.1
13 218414_s_at	NUDE1	-1.90	7.84E-16	2.59E-12	-0.91	-9.50	16p13.11
14 229215_at	ASCL2	-6.84	1.68E-15	5.05E-12	-0.92	-9.47	11p15.5
15 227224_at	FLJ25604	-3.52	6.44E-15	1.77E-11	-0.91	-9.37	1q24.2
16 231310_at		2.60	5.72E-12	5.90E-09	1.01	9.27	
17 232636_at	DKFZp547M2010	-10.00	1.33E-14	2.92E-11	-0.95	-9.27	Xq27.3
18 203973_s_at	CEBPD	2.15	4.87E-12	5.36E-09	0.99	9.14	8p11.2-p11.1
19 211031_s_at	CYLN2	-7.45	1.95E-14	4.02E-11	-0.91	-9.11	7q11.23
20 218795_at	ACP6	-3.17	9.67E-15	2.46E-11	-0.88	-9.11	1q21
21 204197_s_at	RUNX3	-3.20	1.25E-14	2.92E-11	-0.87	-9.00	1p36
22 242520_s_at		-4.95	4.22E-14	7.75E-11	-0.89	-8.95	
23 224724_at	SULF2	6.66	2.80E-09	9.06E-07	1.28	8.84	20q12-13.2
24 219379_x_at	ZNF358	-3.01	2.63E-14	5.12E-11	-0.85	-8.82	
25 205453_at	HOXB2	4.14	7.83E-11	4.88E-08	0.97	8.70	17q21-q22
26 213779_at	LOC129080	-3.47	9.77E-14	1.54E-10	-0.84	-8.65	22q12.1
27 226352_at		-4.36	7.39E-14	1.22E-10	-0.83	-8.64	
28 211026_s_at	MGLL	-2.49	6.63E-14	1.15E-10	-0.83	-8.63	3q21.3
29 205419_at	EBI2	2.98	4.74E-10	2.15E-07	1.01	8.52	13q32.2
30 204563_at	SELL	2.76	3.19E-10	1.66E-07	0.95	8.38	1q23-q25

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
31	207075_at	CIAS1	2.64	3.84E-10	1.86E-07	0.95	8.33	1q44
32	205944_s_at	CLTCL1	-3.84	3.28E-13	4.92E-10	-0.80	-8.32	22q11.21
33	213915_at	NKG7	-2.95	4.13E-13	5.93E-10	-0.79	-8.26	19q13.33
34	219218_at	FLJ23058	-4.23	1.08E-12	1.43E-09	-0.79	-8.14	17q25.3
35	227185_at		-1.78	8.82E-13	1.21E-09	-0.78	-8.12	
36	212667_at	SPARC	3.29	6.11E-09	1.71E-06	1.06	8.11	5q31.3-q32
37	238365_s_at		-4.76	2.84E-12	3.47E-09	-0.81	-8.08	
38	204661_at	CDW52	2.62	4.36E-10	2.03E-07	0.88	8.01	1p36
39	212463_at		-2.98	1.52E-12	1.93E-09	-0.77	-8.01	
40	227120_at	LOC116113	-2.02	9.18E-11	5.52E-08	-0.84	-8.01	6p21.1
41	34210_at	CDW52	2.79	9.51E-10	3.70E-07	0.89	7.93	1p36
42	209822_s_at	VLDLR	-4.04	3.20E-12	3.64E-09	-0.77	-7.92	9p24
43	229168_at	DKFZp434K0621	-3.30	7.81E-12	7.59E-09	-0.80	-7.88	5q35.3
44	204198_s_at	RUNX3	-3.99	2.96E-12	3.49E-09	-0.75	-7.88	1p36
45	229309_at		5.41	2.19E-08	4.36E-06	1.08	7.82	
46	206788_s_at	CBFB	-1.73	2.75E-11	2.16E-08	-0.78	-7.80	16q22.1
47	201432_at	CAT	-1.76	3.16E-11	2.38E-08	-0.78	-7.78	11p13
48	227856_at	FLJ39370	-3.93	5.07E-12	5.41E-09	-0.74	-7.77	4q25
49	227533_at		-2.24	1.12E-11	1.00E-08	-0.75	-7.72	
50	200985_s_at	CD59	-4.36	6.74E-12	6.74E-09	-0.74	-7.72	11p13

3.3   inv(3) versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205382_s_at	DF	-6.90	1.05E-23	2.35E-19	-1.25	-13.02	19p13.3
2	223534_s_at	RPS6KL1	-2.10	1.42E-14	2.64E-11	-1.13	-10.83	14q24.2
3	202759_s_at	AKAP2	-3.56	4.97E-17	3.22E-13	-1.03	-10.53	9q31-q33
4	210115_at	RPL39L	-8.93	5.75E-17	3.22E-13	-1.00	-10.18	3q27
5	228161_at	RAB32	-2.26	3.85E-17	3.22E-13	-0.97	-10.10	6q24.2
6	211709_s_at	SCGF	-3.88	3.26E-11	1.46E-08	-1.13	-9.97	19q13.3
7	212318_at	TRN-SR	-2.36	1.92E-14	2.87E-11	-1.01	-9.96	7q32.2
8	223703_at	CDA017	-2.86	6.39E-16	2.04E-12	-0.97	-9.93	10q23.1
9	242621_at	FLJ32468	-1.54	1.59E-14	2.64E-11	-1.00	-9.92	7q22.1
10	205131_x_at	SCGF	-7.32	8.67E-17	3.88E-13	-0.95	-9.90	19q13.3
11	212953_x_at	CALR	-2.91	1.77E-16	6.62E-13	-0.95	-9.83	19p13.3-p13.2
12	200700_s_at	KDELR2	-2.52	3.93E-15	8.80E-12	-0.96	-9.77	7p22.2
13	203949_at	MPO	-4.18	1.78E-13	1.99E-10	-0.99	-9.70	17q23.1
14	214575_s_at	AZU1	-6.66	8.62E-16	2.21E-12	-0.92	-9.57	19p13.3
15	231300_at	LOC90835	-3.10	1.11E-14	2.25E-11	-0.93	-9.45	16p11.2
16	210783_x_at	SCGF	-6.82	8.90E-16	2.21E-12	-0.91	-9.45	19q13.3
17	203948_s_at	MPO	-5.17	1.92E-13	2.04E-10	-0.92	-9.19	17q23.1
18	205248_at	C21orf5	-1.92	4.97E-13	4.84E-10	-0.91	-9.03	21q22.2
19	202185_at	PLOD3	-2.00	2.36E-12	1.89E-09	-0.93	-9.02	7q22
20	200654_at	P4HB	-2.40	5.53E-11	2.29E-08	-0.98	-9.00	17q25
21	204921_at	GAS8	-3.13	1.65E-14	2.64E-11	-0.85	-8.89	16q24.3
22	202760_s_at	AKAP2	-4.47	1.34E-13	1.57E-10	-0.87	-8.85	9q31-q33
23	224841_x_at		1.53	3.84E-09	5.81E-07	1.07	8.83	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
24	204647_at	HOMER3	-4.41	3.11E-14	4.36E-11	-0.84	-8.80	19p13.11
25	224886_at	STUB1	-1.81	2.17E-12	1.80E-09	-0.89	-8.79	16p13.3
26	230044_at		-2.96	7.03E-12	4.63E-09	-0.91	-8.79	
27	230259_at		-1.66	7.17E-11	2.68E-08	-0.95	-8.78	
28	231736_x_at	MGST1	-3.78	6.77E-12	4.59E-09	-0.90	-8.77	12p12.3-p12.1
29	201186_at	LRPAP1	-2.55	6.42E-13	5.75E-10	-0.86	-8.65	4p16.3
30	204301_at	KIAA0711	-9.40	9.84E-14	1.30E-10	-0.84	-8.65	8p23.2
31	208689_s_at	RPN2	-2.01	3.95E-10	9.52E-08	-0.95	-8.60	20q12-q13.1
32	214315_x_at	CALR	-2.04	1.12E-11	6.57E-09	-0.88	-8.57	19p13.3-p13.2
33	204548_at	STAR	-9.71	1.32E-13	1.57E-10	-0.83	-8.57	8p11.2
34	224741_x_at		1.52	5.30E-09	7.37E-07	1.02	8.56	
35	221739_at	IL27w	-1.81	5.71E-10	1.25E-07	-0.95	-8.52	19p13.3
36	211048_s_at	ERP70	-2.54	2.04E-13	2.08E-10	-0.82	-8.51	7q35
37	233955_x_at	HSPC195	3.20	1.69E-07	1.17E-05	1.26	8.43	5q31.3
38	225010_at	D10S170	1.85	3.33E-09	5.22E-07	0.97	8.37	10q21
39	239656_at		-2.19	3.51E-12	2.45E-09	-0.83	-8.37	
40	208308_s_at	GPI	-2.28	1.00E-09	2.08E-07	-0.92	-8.32	19q13.1
41	227432_s_at	INSR	-2.55	9.60E-11	3.36E-08	-0.87	-8.27	19p13.3-p13.2
42	224918_x_at	MGST1	-3.43	2.52E-10	6.97E-08	-0.88	-8.27	12p12.3-p12.1
43	202487_s_at	H2AV	-1.91	9.08E-09	1.09E-06	-0.98	-8.25	7p13
44	217225_x_at	LOC283820	-1.79	1.49E-10	4.97E-08	-0.87	-8.24	16p13.13
45	226789_at		-2.33	1.17E-11	6.70E-09	-0.82	-8.21	
46	230480_at	HIWI2	-3.24	6.07E-13	5.67E-10	-0.79	-8.20	11q21
47	209836_x_at	MGC5178	-1.81	2.73E-10	7.37E-08	-0.87	-8.20	16p12.1
48	201004_at	SSR4	-1.81	1.56E-11	8.12E-09	-0.82	-8.16	Xq28
49	240672_at		-1.54	2.12E-12	1.80E-09	-0.79	-8.14	
50	240443_at		-1.74	1.55E-11	8.12E-09	-0.81	-8.12	

3.4 t(15;17) versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	-10.73	6.59E-39	1.59E-34	-1.98	-20.66	6p21.3
2	211474_s_at	SERPINB6	-4.87	1.86E-30	2.25E-26	-1.55	-16.18	6p25
3	209732_at	CLECSF2	-33.59	4.68E-28	3.77E-24	-1.64	-16.06	12p13-p12
4	214450_at	CTSW	8.57	4.43E-13	4.79E-11	2.57	16.03	11q13.1
5	38487_at	STAB1	10.15	1.20E-12	1.18E-10	2.68	15.65	3p21.31
6	204425_at	ARHGAP4	-17.49	1.39E-27	8.41E-24	-1.53	-15.46	Xq28
7	221004_s_at	ITM2C	5.41	2.38E-13	2.73E-11	2.24	15.44	2q37
8	212953_x_at	CALR	3.12	1.47E-13	1.77E-11	2.01	14.81	19p13.3-p13.2
9	209619_at	CD74	-4.79	5.24E-21	4.87E-18	-1.50	-14.59	5q32
10	201923_at	PRDX4	-6.70	4.87E-27	2.35E-23	-1.39	-14.52	Xp22.13
11	208306_x_at	HLA-DRB4	-7.49	1.29E-26	5.17E-23	-1.38	-14.39	6p21.3
12	205771_s_at	AKAP7	-8.84	2.49E-26	8.59E-23	-1.38	-14.32	6q23
13	209312_x_at	HLA-DRB1	-7.02	3.98E-26	1.20E-22	-1.37	-14.24	6p21.3
14	201137_s_at	HLA-DPB1	-11.67	4.78E-25	1.15E-21	-1.39	-14.10	6p21.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
15	217478_s_at	HLA-DMA	-5.66	3.09E-25	8.29E-22	-1.31	-13.68	6p21.3
16	200931_s_at	VCL	-3.69	4.10E-24	9.01E-21	-1.30	-13.44	10q22.1-q23
17	204670_x_at	HLA-DRB5	-5.67	6.80E-22	9.11E-19	-1.31	-13.25	6p21.3
18	227353_at	EVER2	-3.66	7.95E-22	1.01E-18	-1.31	-13.24	17q25.3
19	204661_at	CDW52	-21.19	6.93E-23	1.29E-19	-1.29	-13.05	1p36
20	238022_at		6.26	9.58E-12	7.65E-10	1.92	13.00	
21	209288_s_at	CDC42EP3	-7.86	1.01E-23	2.04E-20	-1.24	-12.99	2p21
22	200654_at	P4HB	2.04	4.76E-15	8.84E-13	1.46	12.88	17q25
23	217848_s_at	PP	-3.29	1.17E-20	9.72E-18	-1.26	-12.71	10q11.1-q24
24	211991_s_at	HLA-DPA1	-17.79	5.77E-22	8.67E-19	-1.25	-12.64	6p21.3
25	201719_s_at	EPB41L2	-11.63	6.10E-22	8.67E-19	-1.23	-12.54	6q23
26	208982_at	PECAM1	-4.98	1.27E-22	2.19E-19	-1.20	-12.53	17q23
27	203948_s_at	MPO	2.62	1.47E-17	5.58E-15	1.29	12.43	17q23.1
28	34210_at	CDW52	-26.61	1.88E-21	2.16E-18	-1.23	-12.41	1p36
29	236554_x_at	EVER2	-3.45	3.58E-21	3.76E-18	-1.20	-12.37	17q25.3
30	203535_at	S100A9	-7.50	4.64E-22	7.47E-19	-1.18	-12.29	1q21
31	213587_s_at	LOC155066	-5.24	2.40E-21	2.63E-18	-1.20	-12.23	7q36.1
32	205624_at	CPA3	6.80	7.28E-12	6.00E-10	1.63	12.18	3q21-q25
33	221059_s_at	CHST6	-4.81	8.71E-22	1.05E-18	-1.16	-12.14	16q22
34	228113_at	STAT3	-3.88	3.84E-21	3.78E-18	-1.17	-12.08	17q21
35	224918_x_at	MGST1	2.47	4.93E-14	7.00E-12	1.38	12.07	12p12.3-p12.1
36	217716_s_at	SEC61A1	2.09	9.63E-12	7.65E-10	1.62	12.04	3q21.3
37	221865_at	DKFZp547P234	-3.10	1.39E-20	1.12E-17	-1.15	-11.91	9q33.1
38	227598_at	LOC113763	-3.86	3.91E-21	3.78E-18	-1.13	-11.83	7q35
39	201522_x_at	SNRPN	-3.86	3.58E-15	7.09E-13	-1.28	-11.80	15q12
40	204362_at	SCAP2	-10.33	7.84E-21	7.01E-18	-1.14	-11.80	7p21-p15
41	205663_at	PCBP3	4.02	9.90E-11	6.03E-09	1.81	11.76	21q22.3
42	231736_x_at	MGST1	2.65	8.34E-13	8.43E-11	1.39	11.67	12p12.3-p12.1
43	225639_at	SCAP2	-9.34	1.14E-20	9.72E-18	-1.11	-11.62	7p21-p15
44	215193_x_at	HLA-DRB1	-6.71	4.49E-20	3.39E-17	-1.12	-11.60	6p21.3
45	204046_at	PLCB2	-5.34	4.94E-20	3.52E-17	-1.12	-11.58	15q15
46	232617_at	CTSS	-5.56	5.25E-20	3.62E-17	-1.13	-11.58	1q21
47	223280_x_at	MS4A6A	-17.22	1.88E-19	1.20E-16	-1.16	-11.53	11q12.1
48	203299_s_at	AP1S2	-4.00	2.23E-20	1.73E-17	-1.10	-11.49	Xp22.31
49	230264_s_at	AP1S2	-5.59	4.96E-20	3.52E-17	-1.11	-11.46	Xp22.31
50	241742_at	PRAM-1	-7.38	1.34E-19	8.72E-17	-1.11	-11.39	19p13.2

3.5 t(8;21) versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225615_at	LOC126917	-6.21	2.45E-21	4.69E-17	-1.14	-11.93	1p36.13
2	224764_at	ARHGAP10	-6.00	3.05E-21	4.69E-17	-1.14	-11.91	10
3	201944_at	HEXB	-2.53	3.42E-19	3.50E-15	-1.05	-10.97	5q13
4	200788_s_at	PEA15	-2.30	9.17E-17	2.17E-13	-1.07	-10.77	1q21.1

#	Probe	Gene					
5	204494_s_at	DKFZP434H132	-3.15	1.00E-18	7.67E-15	-1.03	-10.76 15q22.33
6	215087_at		-3.23	1.50E-18	9.23E-15	-1.03	-10.72
7	209500_x_at	TNFSF13	-3.17	2.95E-18	1.47E-14	-1.03	-10.66 17p13.1
8	221581_s_at	WBSCR5	-5.63	3.36E-18	1.47E-14	-1.03	-10.63 7q11.23
9	208890_s_at	PLXNB2	-3.57	6.32E-18	2.16E-14	-1.02	-10.60 22q13.33
10	210314_x_at	TNFSF13	-3.73	1.52E-17	4.25E-14	-1.02	-10.53 17p13.1
11	238077_at	MGC27385	-3.41	5.29E-18	2.03E-14	-1.00	-10.47 3p21.1
12	201425_at	ALDH2	-7.89	1.20E-17	3.67E-14	-1.01	-10.43 12q24.2
13	220974_x_at	BA108L7.2	-4.27	7.46E-17	1.91E-13	-1.02	-10.41 10q24.31
14	227279_at	MGC15737	-2.41	1.39E-15	1.94E-12	-0.96	-9.83 Xq22.1
15	204495_s_at	DKFZP434H132	-3.01	1.81E-16	3.97E-13	-0.94	-9.79 15q22.33
16	201105_at	LGALS1	-4.58	3.24E-16	6.63E-13	-0.94	-9.75 22q13.1
17	205639_at	AOAH	-4.24	9.54E-16	1.63E-12	-0.95	-9.75 7p14-p12
18	201360_at	CST3	-3.74	1.17E-15	1.83E-12	-0.95	-9.73 20p11.21
19	226865_at		-5.11	5.19E-16	9.95E-13	-0.95	-9.71
20	220066_at	CARD15	-6.40	5.68E-16	1.03E-12	-0.91	-9.54 16p12-q21
21	200838_at	CTSB	-2.84	1.19E-15	1.83E-12	-0.92	-9.50 8p22
22	206120_at	CD33	-4.35	1.32E-15	1.92E-12	-0.90	-9.39 19q13.3
23	227276_at	TEM7R	-2.75	2.11E-15	2.70E-12	-0.90	-9.38 10p12.1
24	207075_at	CIAS1	-3.91	1.63E-15	2.17E-12	-0.90	-9.38 1q44
25	201850_at	CAPG	-5.16	3.03E-15	3.72E-12	-0.91	-9.35 2cen-q24
26	201887_at	IL13RA1	-3.15	4.60E-15	5.44E-12	-0.88	-9.20 Xq24
27	240572_s_at		-3.62	5.33E-15	6.07E-12	-0.87	-9.12
28	201596_x_at	KRT18	-9.57	9.31E-15	1.02E-11	-0.89	-9.11 12q13
29	224393_s_at	CECR6	-8.98	1.63E-14	1.73E-11	-0.91	-9.11
30	217226_s_at	BA108L7.2	-2.91	3.09E-14	3.06E-11	-0.87	-8.99 10q24.31
31	223398_at	MGC11115	-2.54	3.92E-14	3.47E-11	-0.88	-8.99 9q22.2
32	203017_s_at	SSX2IP	-2.61	3.10E-13	2.06E-10	-0.90	-8.98
33	207839_s_at	LOC51754	-2.67	5.30E-11	1.56E-08	-0.99	-8.96 9p13.1
34	214835_s_at	SUCLG2	-3.35	4.18E-14	3.56E-11	-0.87	-8.94 3p14.2
35	212828_at	SYNJ2	-2.60	3.42E-14	3.29E-11	-0.86	-8.92 6q25.3
36	212895_s_at	ABR	-2.69	1.23E-13	8.80E-11	-0.87	-8.87 17p13.3
37	212993_at	SAP18	-5.24	2.15E-14	2.20E-11	-0.85	-8.84 13q11
38	223132_s_at	TRIM8	-2.39	3.76E-14	3.47E-11	-0.85	-8.82 10q24.3
39	227995_at		-6.99	7.53E-14	5.78E-11	-0.89	-8.81
40	225245_x_at	H2AFJ	-3.51	3.96E-14	3.47E-11	-0.84	-8.78 12p12
41	224049_at	KCNK17	-2.80	5.16E-14	4.06E-11	-0.85	-8.74 6p21.1
42	202670_at	MAP2K1	-2.34	5.03E-14	4.06E-11	-0.84	-8.74 15q22.1-q22.33
43	211084_x_at	PRKCN	-3.82	6.03E-12	2.64E-09	-0.90	-8.69 2p21
44	219690_at	FLJ22573	-2.40	5.15E-14	4.06E-11	-0.83	-8.68 19q13.11
45	212423_at	FLJ90798	-4.03	8.22E-14	6.16E-11	-0.83	-8.65 10q22.3
46	219165_at	PDLIM2	-2.76	4.30E-13	2.54E-10	-0.84	-8.59 8p21.2
47	201952_at	ALCAM	-2.81	4.16E-13	2.50E-10	-0.84	-8.56 3q13.1
48	241370_at		-2.43	1.31E-13	9.14E-11	-0.82	-8.54
49	205419_at	EBI2	-4.18	1.20E-13	8.78E-11	-0.81	-8.50 13q32.2
50	204487_s_at	KCNQ1	-6.32	3.22E-13	2.06E-10	-0.82	-8.49 11p15.5

Table 4

4. All-Pairs (AP)

4.1   11q23 versus inv(16)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213737_x_at		3.73	1.13E-15	1.73E-11	2.10	13.96	
2	200665_s_at	SPARC	-16.71	3.03E-13	1.32E-09	-2.29	-13.74	5q31.3-q32
3	200953_s_at	CCND2	-4.22	1.13E-15	1.73E-11	-1.89	-13.24	12p13
4	214651_s_at	HOXA9	24.48	6.34E-14	4.83E-10	2.09	12.83	7p15-p14
5	202746_at	ITM2A	-15.51	1.87E-12	5.21E-09	-2.15	-12.76	Xq13.3-Xq21.2
6	202747_s_at	ITM2A	-15.29	3.80E-12	7.25E-09	-2.03	-12.22	Xq13.3-Xq21.2
7	231310_at		-4.48	1.13E-14	1.15E-10	-1.64	-11.74	
8	200951_s_at	CCND2	-5.06	4.26E-13	1.63E-09	-1.72	-11.64	12p13
9	202551_s_at	CRIM1	-4.41	2.93E-13	1.32E-09	-1.63	-11.30	2p21
10	206847_s_at	HOXA7	6.89	1.31E-12	4.43E-09	1.67	10.96	7p15-p14
11	227567_at		5.37	2.91E-13	1.32E-09	1.58	10.93	
12	201497_x_at	MYH11	-25.07	1.61E-10	1.34E-07	-2.11	-10.83	16p13.13-p13.12
13	205453_at	HOXB2	-7.71	7.13E-12	1.28E-08	-1.64	-10.82	17q21-q22
14	235753_at		13.56	9.87E-12	1.51E-08	1.80	10.62	
15	201496_x_at	MYH11	-6.90	6.26E-11	7.35E-08	-1.73	-10.60	16p13.13-p13.12
16	212667_at	SPARC	-8.20	5.65E-11	6.89E-08	-1.65	-10.40	5q31.3-q32
17	224049_at	KCNK17	-4.41	9.00E-11	9.46E-08	-1.66	-10.31	6p21.1
18	213147_at	HOXA10	6.19	3.53E-12	7.19E-09	1.50	10.20	7p15-p14
19	229215_at	ASCL2	10.61	2.45E-11	3.40E-08	1.55	9.93	11p15.5
20	203949_at	MPO	-3.22	2.23E-12	5.29E-09	-1.38	-9.79	17q23.1
21	209905_at	HOXA9	81.21	7.73E-11	8.74E-08	1.69	9.76	7p15-p14
22	226517_at	BCAT1	-10.39	6.14E-10	3.82E-07	-1.62	-9.66	12pter-q12
23	202931_x_at	BIN1	-2.97	2.31E-12	5.29E-09	-1.32	-9.58	2q14
24	213908_at		15.53	1.14E-10	1.10E-07	1.59	9.54	
25	201830_s_at	NET1	-4.02	1.63E-10	1.34E-07	-1.45	-9.52	10p15
26	223471_at	RAB3IP	3.55	8.58E-12	1.45E-08	1.35	9.50	
27	201029_s_at	CD99	-1.93	2.43E-12	5.29E-09	-1.31	-9.48	Xp22.32
28	224952_at	DKFZP564D166	3.54	1.88E-12	5.21E-09	1.27	9.31	17q23.3
29	204082_at	PBX3	5.48	1.81E-10	1.45E-07	1.49	9.25	9q33-q34
30	228058_at	LOC124220	-5.44	9.13E-12	1.47E-08	-1.27	-9.16	16p13.3
31	225831_at	LOC148894	-3.50	2.57E-10	1.96E-07	-1.35	-9.05	1p36.11
32	205330_at	MN1	-16.11	4.51E-09	1.52E-06	-1.71	-9.04	22q12.1
33	202370_s_at	CBFB	3.04	1.34E-10	1.20E-07	1.36	9.03	16q22.1
34	225102_at	LOC152009	5.50	1.44E-10	1.26E-07	1.34	8.98	3q21.3
35	210139_s_at	PMP22	-8.84	3.42E-09	1.26E-06	-1.52	-8.92	17p12-p11.2
36	211012_s_at	PML	-2.72	4.71E-11	5.99E-08	-1.22	-8.76	15q22
37	200602_at	APP	-6.17	1.23E-10	1.14E-07	-1.24	-8.73	21q21.3

38	203733_at	MYLE	3.27	8.06E-11	8.78E-08	1.24	8.72	16p13.2
39	228496_s_at	CRIM1	-2.82	1.15E-10	1.10E-07	-1.23	-8.70	2p21
40	226137_at		-3.57	2.49E-09	1.07E-06	-1.38	-8.69	
41	214452_at	BCAT1	-4.11	1.17E-09	6.73E-07	-1.30	-8.60	12pter-q12
42	203329_at	PTPRM	-5.80	7.33E-09	2.17E-06	-1.48	-8.60	18p11.2
43	241706_at	LOC144402	6.03	4.36E-10	2.96E-07	1.26	8.52	12q11
44	213150_at	HOXA10	11.20	1.28E-09	7.06E-07	1.38	8.51	7p15-p14
45	201828_x_at	CXX1	2.80	1.75E-11	2.54E-08	1.15	8.51	Xq26
46	202265_at	BMI1	3.17	4.25E-10	2.95E-07	1.25	8.48	10p11.23
47	210006_at	DKFZP564O243	2.23	5.26E-10	3.42E-07	1.26	8.46	3p21.1
48	225285_at		-9.01	3.35E-09	1.26E-06	-1.31	-8.44	
49	242738_s_at		-2.35	5.69E-10	3.62E-07	-1.22	-8.43	
50	218966_at	MYO5C	-2.93	2.74E-09	1.13E-06	-1.28	-8.36	15q21

4.2   11q23 versus inv(3)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204082_at	PBX3	8.05	2.96E-11	4.56E-07	1.56	9.79	9q33-q34
2	226789_at		3.17	7.24E-11	4.56E-07	1.31	8.77	
3	225344_at	ERAP140	-4.35	2.49E-07	4.83E-05	-1.77	-8.74	6q22.33
4	214651_s_at	HOXA9	4.34	4.49E-11	4.56E-07	1.28	8.67	7p15-p14
5	222982_x_at	SLC38A2	-1.93	7.96E-10	1.84E-06	-1.31	-8.55	12q
6	213893_x_at	PMS2L5	2.34	7.87E-11	4.56E-07	1.26	8.53	7q11-q22
7	236398_s_at		6.39	2.46E-10	1.12E-06	1.29	8.52	
8	235753_at		4.79	2.97E-10	1.12E-06	1.27	8.39	
9	233955_x_at	HSPC195	-4.27	9.34E-09	6.01E-06	-1.34	-8.38	5q31.3
10	210006_at	DKFZP564O243	2.30	3.38E-10	1.12E-06	1.26	8.35	3p21.1
11	235199_at		-3.81	2.13E-07	4.41E-05	-1.54	-8.32	
12	203733_at	MYLE	2.89	5.18E-10	1.33E-06	1.22	8.12	16p13.2
13	212318_at	TRN-SR	2.59	4.46E-10	1.29E-06	1.21	8.10	7q32.2
14	202053_s_at	ALDH3A2	2.81	1.73E-09	2.56E-06	1.22	7.94	17p11.2
15	214643_x_at	BIN1	-4.34	2.80E-07	5.15E-05	-1.43	-7.94	2q14
16	209905_at	HOXA9	6.89	1.61E-09	2.56E-06	1.21	7.93	7p15-p14
17	228083_at	CACNA2D4	8.25	1.77E-09	2.56E-06	1.21	7.91	12p13.33
18	225386_s_at	LOC92906	6.11	1.05E-09	2.22E-06	1.17	7.84	2p22.2
19	223703_at	CDA017	3.76	3.59E-09	3.24E-06	1.21	7.80	10q23.1
20	200602_at	APP	-9.73	7.82E-07	1.01E-04	-1.48	-7.75	21q21.3
21	212782_x_at	POLR2J	2.42	3.77E-09	3.24E-06	1.15	7.66	7q11.2
22	208116_s_at	MAN1A1	-4.72	9.63E-07	1.16E-04	-1.47	-7.63	6q22
23	208967_s_at	AK2	3.86	8.89E-09	5.89E-06	1.21	7.62	1p34
24	215667_x_at	PMS2L5	1.93	2.43E-09	3.01E-06	1.13	7.62	7q11-q22
25	225389_at	BTBD6	2.27	1.62E-09	2.56E-06	1.12	7.60	14q32
26	221036_s_at	PSFL	2.03	1.74E-09	2.56E-06	1.12	7.57	15q21.3
27	214430_at	GLA	2.10	2.07E-09	2.82E-06	1.11	7.51	Xq22
28	206440_at	LIN7A	8.97	8.85E-09	5.89E-06	1.16	7.49	12q21
29	230051_at		-4.16	5.08E-07	7.64E-05	-1.32	-7.48	

30	209836_x_at	MGC5178	2.05	2.47E-09	3.01E-06	1.10	7.47	16p12.1
31	202961_s_at	ATP5J2	2.24	5.44E-09	4.35E-06	1.11	7.45	7q22.1
32	212174_at	AK2	3.70	6.56E-09	4.90E-06	1.13	7.45	1p34
33	213370_s_at	SFMBT	1.98	3.04E-09	3.24E-06	1.10	7.44	3p21.31
34	222996_s_at	HSPC195	-4.05	7.45E-07	9.81E-05	-1.34	-7.43	5q31.3
35	202054_s_at	ALDH3A2	4.23	2.86E-09	3.24E-06	1.09	7.42	17p11.2
36	224516_s_at	HSPC195	-5.00	2.99E-07	5.38E-05	-1.26	-7.41	5q31.3
37	206847_s_at	HOXA7	2.83	3.35E-09	3.24E-06	1.10	7.41	7p15-p14
38	201186_at	LRPAP1	3.21	7.87E-09	5.70E-06	1.12	7.39	4p16.3
39	219126_at	XAP135	1.82	3.30E-09	3.24E-06	1.09	7.38	6q27
40	219991_at	SLC2A9	2.18	5.75E-09	4.44E-06	1.11	7.38	4p16-p15.3
41	202605_at	GUSB	3.16	4.47E-09	3.70E-06	1.10	7.37	7q21.11
42	213908_at		3.92	1.51E-08	8.34E-06	1.15	7.37	
43	223207_x_at	PHP14	1.80	3.42E-09	3.24E-06	1.09	7.36	9q34.3
44	220924_s_at	SLC38A2	-1.62	3.76E-09	3.24E-06	-1.08	-7.34	12q
45	200654_at	P4HB	2.25	8.68E-09	5.89E-06	1.09	7.28	17q25
46	206478_at	KIAA0125	-13.74	3.61E-06	2.61E-04	-1.64	-7.27	14q32.33
47	218041_x_at	SLC38A2	-1.65	1.58E-08	8.49E-06	-1.09	-7.21	12q
48	214453_s_at	IFI44	-4.71	1.66E-06	1.59E-04	-1.34	-7.18	1p31.1
49	231300_at	LOC90835	3.98	2.03E-08	9.99E-06	1.11	7.18	16p11.2
50	209696_at	FBP1	4.25	3.05E-08	1.29E-05	1.14	7.17	9q22.3

4.3 11q23 versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	221004_s_at	ITM2C	-11.20	1.59E-14	7.61E-11	-2.87	-17.09	2q37
2	38487_at	STAB1	-16.01	3.30E-13	5.91E-10	-2.90	-16.10	3p21.31
3	203948_s_at	MPO	-6.05	4.56E-20	1.14E-15	-2.14	-15.28	17q23.1
4	205624_at	CPA3	-35.38	6.12E-12	5.68E-09	-3.00	-14.74	3q21-q25
5	212953_x_at	CALR	-3.21	1.82E-14	7.61E-11	-2.20	-14.27	19p13.3-p13.2
6	214450_at	CTSW	-6.21	4.49E-14	1.36E-10	-2.19	-14.03	11q13.1
7	200953_s_at	CCND2	-6.31	2.30E-12	2.80E-09	-2.26	-13.45	12p13
8	214651_s_at	HOXA9	234.13	3.24E-14	1.16E-10	2.39	13.42	7p15-p14
9	203949_at	MPO	-4.22	1.85E-17	2.31E-13	-1.87	-13.25	17q23.1
10	238022_at		-6.27	2.35E-12	2.80E-09	-1.99	-12.44	
11	206871_at	ELA2	-4.10	1.64E-16	1.37E-12	-1.75	-12.43	19p13.3
12	233072_at	KIAA1857	-12.50	6.74E-11	3.12E-08	-2.26	-12.31	9q34
13	213147_at	HOXA10	23.75	2.86E-13	5.88E-10	2.04	12.19	7p15-p14
14	201029_s_at	CD99	-2.27	1.40E-15	8.79E-12	-1.62	-11.54	Xp22.32
15	204150_at	STAB1	-19.83	3.61E-10	1.14E-07	-2.25	-11.52	3p21.31
16	206847_s_at	HOXA7	9.16	4.76E-13	7.95E-10	1.78	11.45	7p15-p14
17	210788_s_at	retSDR4	-2.58	1.11E-11	8.39E-09	-1.79	-11.35	14q22.3
18	209448_at	HTATIP2	10.11	1.01E-12	1.58E-09	1.80	11.31	11p15.1
19	200951_s_at	CCND2	-7.13	1.97E-10	7.68E-08	-1.93	-11.10	12p13
20	205663_at	PCBP3	-3.88	3.71E-11	1.90E-08	-1.79	-11.09	21q22.3
21	212509_s_at		-6.33	1.39E-10	6.21E-08	-1.87	-11.03	

22 206761_at	TACTILE	-25.65	1.23E-09	2.84E-07	-2.20	-10.83	3q13.13
23 235753_at		16.24	7.41E-12	6.19E-09	1.86	10.77	
24 231736_x_at	MGST1	-2.95	1.27E-13	2.89E-10	-1.53	-10.74	12p12.3-p12.1
25 213587_s_at	LOC155066	7.68	8.23E-12	6.65E-09	1.74	10.58	7q36.1
26 224918_x_at	MGST1	-2.77	4.90E-14	1.36E-10	-1.49	-10.57	12p12.3-p12.1
27 201596_x_at	KRT18	-9.08	5.27E-10	1.50E-07	-1.81	-10.49	12q13
28 205349_at	GNA15	-3.93	1.96E-12	2.73E-09	-1.53	-10.47	19p13.3
29 217848_s_at	PP	3.79	3.05E-13	5.88E-10	1.50	10.44	10q11.1-q24
30 201522_x_at	SNRPN	4.60	7.40E-14	1.85E-10	1.46	10.39	15q12
31 205771_s_at	AKAP7	9.76	6.69E-12	5.78E-09	1.62	10.38	6q23
32 200952_s_at	CCND2	-3.93	2.46E-10	8.91E-08	-1.67	-10.25	12p13
33 225532_at	LOC91768	-5.23	7.13E-10	1.88E-07	-1.73	-10.17	18q11.1
34 225386_s_at	LOC92906	35.64	2.81E-11	1.67E-08	1.73	10.16	2p22.2
35 221253_s_at	MGC3178	-3.09	1.65E-10	7.12E-08	-1.61	-10.14	6p24.3
36 218404_at	SNX10	6.55	1.28E-11	9.41E-09	1.55	10.03	7p15.2
37 204425_at	ARHGAP4	15.70	3.11E-11	1.80E-08	1.63	9.99	Xq28
38 204082_at	PBX3	8.58	2.56E-11	1.66E-08	1.58	9.93	9q33-q34
39 209905_at	HOXA9	701.37	6.10E-11	2.94E-08	1.77	9.88	7p15-p14
40 217716_s_at	SEC61A1	-1.97	6.02E-12	5.68E-09	-1.43	-9.86	3q21.3
41 213571_s_at	EIF4EL3	2.56	1.14E-12	1.67E-09	1.41	9.85	2q37.1
42 225570_at	SLC41A1	3.46	2.26E-12	2.80E-09	1.41	9.81	1q32.1
43 223663_at	FLJ37970	7.30	4.86E-12	5.07E-09	1.41	9.71	11q12.3
44 241383_at		-4.20	3.65E-09	6.44E-07	-1.74	-9.68	
45 219837_s_at	C17	-67.10	8.83E-09	1.18E-06	-2.02	-9.65	4p16-p15
46 210140_at	CST7	-6.71	1.39E-09	3.08E-07	-1.61	-9.65	20p11.21
47 208852_s_at	CANX	-2.25	6.37E-11	3.01E-08	-1.43	-9.58	5q35
48 216417_x_at	HOXB9	3.56	4.25E-12	4.63E-09	1.38	9.57	17q21.3
49 212813_at	JAM3	-4.92	4.22E-09	7.05E-07	-1.69	-9.54	11q25
50 202746_at	ITM2A	-18.16	8.43E-09	1.14E-06	-1.85	-9.52	Xq13.3-Xq21.2

4.4   11q23 versus t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1 214651_s_at		HOXA9	206.03	3.28E-14	1.03E-09	2.38	13.41	7p15-p14
2 221581_s_at		WBSCR5	9.58	9.94E-14	1.56E-09	1.98	12.37	7q11.23
3 213147_at		HOXA10	15.43	4.12E-13	3.22E-09	1.91	11.80	7p15-p14
4 206847_s_at		HOXA7	8.17	9.28E-13	5.26E-09	1.83	11.41	7p15-p14
5 235753_at			14.64	8.54E-12	2.97E-08	1.82	10.68	
6 201105_at		LGALS1	6.65	1.61E-12	7.21E-09	1.54	10.34	22q13.1
7 227853_at			3.55	1.68E-13	1.76E-09	1.47	10.30	
8 209905_at		HOXA9	614.03	6.13E-11	1.37E-07	1.77	9.87	7p15-p14
9 203949_at		MPO	-3.89	1.01E-12	5.26E-09	-1.40	-9.82	17q23.1
10 210314_x_at		TNFSF13	4.55	4.40E-12	1.72E-08	1.42	9.72	17p13.1
11 213908_at			15.54	1.15E-10	2.13E-07	1.61	9.55	
12 213150_at		HOXA10	54.55	2.66E-10	3.78E-07	1.61	9.25	7p15-p14

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
13	209500_x_at	TNFSF13	3.85	4.68E-11	1.22E-07	1.37	9.17	17p13.1
14	204082_at	PBX3	6.31	5.89E-11	1.37E-07	1.34	9.03	9q33-q34
15	205639_at	AOAH	5.46	8.40E-11	1.75E-07	1.29	8.80	7p14-p12
16	228365_at	LOC144402	7.86	5.32E-10	6.36E-07	1.42	8.80	12q11
17	208890_s_at	PLXNB2	3.97	9.29E-11	1.82E-07	1.29	8.76	22q13.33
18	228083_at	CACNA2D4	12.54	7.21E-10	7.06E-07	1.44	8.75	12p13.33
19	201944_at	HEXB	3.38	5.49E-10	6.36E-07	1.39	8.72	5q13
20	218404_at	SNX10	4.18	1.56E-10	2.65E-07	1.29	8.68	7p15.2
21	204202_at	KIAA1023	3.42	1.65E-10	2.65E-07	1.28	8.66	7p22.3
22	225245_x_at	H2AFJ	4.99	2.65E-10	3.78E-07	1.30	8.64	12p12
23	212459_x_at	SUCLG2	3.67	2.89E-11	9.04E-08	1.22	8.63	3p14.2
24	216417_x_at	HOXB9	3.30	4.27E-11	1.22E-07	1.21	8.51	17q21.3
25	223562_at	PARVG	3.18	5.28E-10	6.36E-07	1.25	8.36	22q13.2-q13
26	218217_at	RISC	5.15	1.01E-09	8.75E-07	1.29	8.35	17q23.1
27	203948_s_at	MPO	-4.44	6.12E-10	6.61E-07	-1.23	-8.34	17q23.1
28	228058_at	LOC124220	-6.10	5.49E-09	3.37E-06	-1.29	-8.28	16p13.3
29	241706_at	LOC144402	5.35	8.09E-10	7.45E-07	1.22	8.17	12q11
30	201850_at	CAPG	7.89	3.15E-09	2.10E-06	1.35	8.17	2cen-q24
31	224301_x_at	H2AFJ	4.16	7.21E-10	7.06E-07	1.21	8.17	12p12
32	214835_s_at	SUCLG2	3.91	4.04E-10	5.27E-07	1.19	8.16	3p14.2
33	206940_s_at	POU4F1	-33.65	1.84E-07	3.22E-05	-1.76	-8.14	13q21.1-q22
34	212423_at	FLJ90798	5.61	1.08E-09	9.14E-07	1.22	8.14	10q22.3
35	215772_x_at	SUCLG2	3.87	1.69E-10	2.65E-07	1.15	8.09	3p14.2
36	202746_at	ITM2A	-7.27	5.70E-08	1.67E-05	-1.39	-8.08	Xq13.3-Xq21.2
37	238756_at		4.09	1.20E-09	9.93E-07	1.21	8.08	
38	204880_at	MGMT	-2.32	5.45E-09	3.37E-06	-1.23	-8.04	10q26
39	241370_at		3.17	2.09E-09	1.49E-06	1.20	7.94	
40	224415_s_at	HINT2	2.05	3.49E-10	4.75E-07	1.13	7.93	9p13.1
41	228827_at		-103.62	2.83E-07	4.30E-05	-1.80	-7.92	
42	225386_s_at	LOC92906	6.59	6.59E-10	6.88E-07	1.14	7.90	2p22.2
43	200788_s_at	PEA15	2.38	7.77E-10	7.37E-07	1.14	7.87	1q21.1
44	207839_s_at	LOC51754	2.68	5.92E-10	6.61E-07	1.12	7.85	9p13.1
45	206009_at	ITGA9	-3.62	5.12E-08	1.58E-05	-1.28	-7.81	3p21.3
46	211341_at	POU4F1	-150.84	3.58E-07	5.05E-05	-1.74	-7.79	13q21.1-q22
47	56256_at	CGI-40	2.81	1.88E-09	1.37E-06	1.14	7.77	11q23.3
48	217520_x_at	LOC283683	16.90	1.17E-08	5.50E-06	1.38	7.76	15q11.2
49	219478_at	WFDC1	-6.75	1.65E-07	3.09E-05	-1.36	-7.72	16q24.3
50	205774_at	F12	3.18	1.69E-09	1.32E-06	1.11	7.68	5q33-qter

4.5 inv(16) versus inv(3)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	4.74	1.72E-13	4.54E-09	2.41	14.22	17q23.1
2	203948_s_at	MPO	5.13	2.36E-12	2.08E-08	1.89	11.46	17q23.1
3	205382_s_at	DF	5.65	1.05E-12	1.38E-08	1.83	11.19	19p13.3

4 201497_x_at	MYH11	18.46	2.05E-10	7.07E-07	2.06	10.65	16p13.13-p13.12
5 224841_x_at		-1.69	2.14E-10	7.07E-07	-1.76	-10.33	
6 224741_x_at		-1.69	3.09E-10	9.08E-07	-1.76	-10.28	
7 209365_s_at	ECM1	3.28	3.37E-11	2.23E-07	1.54	9.53	1q21
8 210755_at	HGF	6.18	6.96E-10	1.84E-06	1.65	9.44	7q21.1
9 228497_at	FLIPT1	-3.11	8.82E-09	1.17E-05	-1.63	-9.19	1p13.1
10 205718_at	ITGB7	3.07	1.91E-10	7.07E-07	1.44	8.88	12q13.13
11 205131_x_at	SCGF	4.37	1.79E-10	7.07E-07	1.40	8.73	19q13.3
12 217963_s_at	NGFRAP1	-20.39	5.19E-07	1.67E-04	-1.88	-8.49	Xq22.1
13 201496_x_at	MYH11	3.64	1.43E-09	3.16E-06	1.40	8.45	16p13.13-p13.12
14 222862_s_at	AK5	40.65	3.10E-08	2.93E-05	1.61	8.14	1p31
15 236646_at	FLJ31166	3.02	9.63E-10	2.31E-06	1.30	8.12	12p13.31
16 226197_at		2.75	2.51E-09	4.46E-06	1.31	8.04	
17 203074_at	ANXA8	1.80	2.08E-09	4.22E-06	1.30	8.04	10q11.2
18 243244_at		3.90	2.53E-09	4.46E-06	1.29	7.95	
19 202605_at	GUSB	2.22	4.26E-08	3.47E-05	1.30	7.70	7q21.11
20 212358_at	CLIPR-59	15.49	8.58E-08	5.04E-05	1.46	7.63	19q13.12
21 201360_at	CST3	3.63	4.80E-09	7.94E-06	1.22	7.62	20p11.21
22 226697_at	LOC92689	2.52	6.69E-09	1.04E-05	1.22	7.58	4p14
23 201462_at	KIAA0193	-5.29	3.06E-07	1.13E-04	-1.37	-7.57	7p14.3-p14.1
24 241525_at	LOC200772	55.36	1.35E-07	6.48E-05	1.47	7.46	2q37.3
25 210783_x_at	SCGF	4.12	8.13E-09	1.13E-05	1.20	7.46	19q13.3
26 231736_x_at	MGST1	3.57	7.41E-09	1.09E-05	1.19	7.44	12p12.3-p12.1
27 207961_x_at	MYH11	15.00	1.40E-07	6.63E-05	1.43	7.42	16p13.13-p13.12
28 224441_s_at	MGC14793	-3.13	8.20E-08	5.04E-05	-1.24	-7.37	6q16.3
29 205076_s_at	CRA	4.21	4.89E-08	3.77E-05	1.24	7.34	1q12-q21
30 210997_at	HGF	17.75	1.55E-07	6.94E-05	1.38	7.34	7q21.1
31 209975_at	CYP2E1	3.46	4.33E-08	3.47E-05	1.22	7.30	10q24.3-qter
32 224918_x_at	MGST1	3.27	1.58E-08	1.90E-05	1.18	7.29	12p12.3-p12.1
33 201069_at	MMP2	2.83	1.26E-08	1.59E-05	1.17	7.28	16q13-q21
34 202828_s_at	MMP14	5.47	1.26E-07	6.34E-05	1.29	7.25	14q11-q12
35 211709_s_at	SCGF	3.22	3.48E-08	3.08E-05	1.18	7.24	19q13.3
36 202283_at	SERPINF1	4.68	3.61E-08	3.08E-05	1.18	7.18	17p13.1
37 200852_x_at	GNB2	2.10	2.31E-08	2.65E-05	1.15	7.16	7q22
38 201688_s_at	TPD52	-3.31	7.77E-07	2.23E-04	-1.30	-7.14	8q21
39 219308_s_at	AK5	5.75	2.20E-07	9.06E-05	1.32	7.14	1p31
40 239814_at		2.34	2.50E-08	2.75E-05	1.14	7.12	
41 200985_s_at	CD59	-6.95	2.61E-06	5.15E-04	-1.42	-7.09	11p13
42 242621_at	FLJ32468	1.47	2.87E-08	2.81E-05	1.14	7.08	7q22.1
43 202185_at	PLOD3	1.78	2.78E-08	2.81E-05	1.14	7.07	7q22
44 223136_at	AIG-1	-5.06	9.07E-07	2.45E-04	-1.28	-7.05	6q24.1
45 223091_x_at	GL004	-1.53	1.27E-07	6.34E-05	-1.17	-7.04	2q36.3
46 223354_x_at	GL004	-1.62	2.88E-07	1.09E-04	-1.21	-7.04	2q36.3
47 214797_s_at	PCTK3	-2.39	4.15E-07	1.44E-04	-1.22	-7.03	1q31-q32
48 214558_at	GPR12	1.53	4.99E-08	3.77E-05	1.14	7.01	13q12

49 229309_at		4.49	6.27E-08	4.25E-05	1.15	7.01
50 205859_at	LY86	3.30	2.78E-08	2.81E-05	1.12	7.01 6p24.3

4.6 inv(16) versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	12.88	7.26E-18	1.92E-13	3.35	20.08	6p21.3
2	214450_at	CTSW	-8.03	6.77E-13	7.14E-10	-3.05	-15.96	11q13.1
3	38487_at	STAB1	-8.03	2.37E-12	1.95E-09	-3.01	-15.25	3p21.31
4	221004_s_at	ITM2C	-5.22	1.41E-13	3.01E-10	-2.58	-15.04	2q37
5	204661_at	CDW52	33.75	1.67E-13	3.15E-10	2.69	14.74	1p36
6	200654_at	P4HB	-2.30	1.92E-15	1.27E-11	-2.31	-14.63	17q25
7	203535_at	S100A9	9.01	7.53E-16	6.62E-12	2.24	14.32	1q21
8	217478_s_at	HLA-DMA	7.63	2.80E-14	8.72E-11	2.35	14.21	6p21.3
9	209732_at	CLECSF2	30.47	5.76E-13	6.61E-10	2.71	14.20	12p13-p12
10	34210_at	CDW52	43.85	7.27E-13	7.14E-10	2.58	13.90	1p36
11	238022_at		-8.74	2.99E-12	2.25E-09	-2.41	-13.63	
12	209619_at	CD74	5.65	3.24E-16	4.28E-12	2.06	13.52	5q32
13	201923_at	PRDX4	7.22	7.48E-14	1.79E-10	2.16	13.28	Xp22.13
14	205624_at	CPA3	-9.54	1.00E-11	6.01E-09	-2.41	-13.24	3q21-q25
15	204563_at	SELL	9.35	7.30E-13	7.14E-10	2.25	13.07	1q23-q25
16	200931_s_at	VCL	3.96	1.06E-14	5.62E-11	2.01	12.90	10q22.1-q23
17	231310_at		4.74	2.97E-14	8.72E-11	2.04	12.89	
18	209312_x_at	HLA-DRB1	8.89	3.15E-13	4.37E-10	2.06	12.62	6p21.3
19	208306_x_at	HLA-DRB4	9.65	5.23E-13	6.43E-10	2.08	12.60	6p21.3
20	238365_s_at		-10.74	1.01E-10	3.36E-08	-2.50	-12.45	
21	208891_at	DUSP6	7.70	2.11E-14	8.72E-11	1.93	12.44	12q22-q23
22	212953_x_at	CALR	-2.84	2.97E-14	8.72E-11	-1.91	-12.34	19p13.3-p13.2
23	204670_x_at	HLA-DRB5	6.79	3.94E-14	1.04E-10	1.91	12.25	6p21.3
24	205718_at	ITGB7	6.61	6.63E-13	7.14E-10	1.97	12.10	12q13.13
25	205453_at	HOXB2	11.16	1.03E-11	6.03E-09	2.13	11.95	17q21-q22
26	205663_at	PCBP3	-4.69	1.37E-11	7.52E-09	-2.01	-11.85	21q22.3
27	232617_at	CTSS	8.88	1.90E-11	9.29E-09	2.15	11.78	1q21
28	207375_s_at	IL15RA	4.80	1.48E-13	3.01E-10	1.84	11.77	10p15-p14
29	224583_at	COTL1	5.58	3.11E-13	4.37E-10	1.86	11.77	16q23.3
30	221059_s_at	CHST6	6.80	4.13E-12	2.80E-09	1.95	11.67	16q22
31	233072_at	KIAA1857	-7.47	2.04E-10	5.49E-08	-2.19	-11.60	9q34
32	229168_at	DKFZp434K0621	-6.73	3.74E-10	8.88E-08	-2.36	-11.59	5q35.3
33	208982_at	PECAM1	4.84	2.17E-12	1.85E-09	1.88	11.55	17q23
34	224839_s_at	GPT2	-9.02	4.23E-11	1.75E-08	-1.95	-11.41	16q12.1
35	202803_s_at	ITGB2	5.43	5.36E-13	6.43E-10	1.72	11.07	21q22.3
36	223280_x_at	MS4A6A	24.98	9.94E-11	3.36E-08	2.11	11.04	11q12.1
37	201496_x_at	MYH11	10.61	1.13E-11	6.47E-09	1.81	10.98	16p13.13-p13.12
38	211991_s_at	HLA-DPA1	25.17	9.82E-11	3.36E-08	2.05	10.97	6p21.3
39	204150_at	STAB1	-9.71	1.08E-09	2.11E-07	-2.26	-10.94	3p21.31

40 208689_s_at	RPN2	-1.75	1.91E-13	3.36E-10	-1.66	-10.90	20q12-q13.1
41 220798_x_at	FLJ11535	-3.81	7.69E-11	2.82E-08	-1.84	-10.89	19p13.3
42 201497_x_at	MYH11	28.44	1.48E-10	4.48E-08	2.16	10.88	16p13.13-p13.12
43 202917_s_at	S100A8	3.19	3.79E-13	5.01E-10	1.66	10.85	1q21
44 241742_at	PRAM-1	11.60	1.23E-10	3.81E-08	1.97	10.76	19p13.2
45 228046_at	LOC152485	3.03	5.49E-12	3.54E-09	1.72	10.76	4q31.1
46 226878_at		4.19	1.90E-11	9.29E-09	1.77	10.75	
47 238604_at		3.63	2.30E-13	3.79E-10	1.62	10.71	
48 213779_at	LOC129080	-6.64	9.66E-10	1.96E-07	-2.04	-10.68	22q12.1
49 224356_x_at	MS4A6A	25.23	2.22E-10	5.74E-08	2.06	10.62	11q12.1
50 217897_at	FXYD6	3.03	3.34E-11	1.44E-08	1.77	10.62	11q23.3

4.7 inv(16) versus t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1 207075_at	CIAS1	6.59	1.58E-12	1.75E-08	2.20	12.68	1q44
2 208890_s_at	PLXNB2	5.12	3.17E-13	7.15E-09	1.97	12.18	22q13.33
3 205453_at	HOXB2	12.87	7.80E-12	3.24E-08	2.16	12.11	17q21-q22
4 205419_at	EBI2	7.52	3.29E-12	2.73E-08	2.01	11.90	13q32.2
5 205718_at	ITGB7	6.71	4.31E-13	7.15E-09	1.91	11.89	12q13.13
6 224764_at	ARHGAP10	8.78	1.26E-11	4.63E-08	2.02	11.59	10
7 201497_x_at	MYH11	26.12	1.56E-10	2.16E-07	2.14	10.85	16p13.13-p13.12
8 201496_x_at	MYH11	9.21	1.72E-11	5.70E-08	1.80	10.83	16p13.13-p13.12
9 224049_at	KCNK17	4.64	1.11E-10	1.77E-07	1.92	10.69	6p21.1
10 200665_s_at	SPARC	4.28	7.71E-12	3.24E-08	1.63	10.32	5q31.3-q32
11 224724_at	SULF2	26.61	4.15E-10	4.05E-07	1.99	10.28	20q12-13.2
12 218236_s_at	PRKCN	4.73	5.10E-12	3.10E-08	1.59	10.16	2p21
13 218795_at	ACP6	-4.42	3.10E-10	3.26E-07	-1.68	-10.03	1q21
14 201425_at	ALDH2	7.98	2.08E-10	2.50E-07	1.72	10.03	12q24.2
15 201944_at	HEXB	2.26	4.28E-11	1.01E-07	1.57	9.82	5q13
16 201887_at	IL13RA1	4.99	3.14E-10	3.26E-07	1.63	9.67	Xq24
17 201360_at	CST3	5.36	1.21E-10	1.83E-07	1.57	9.65	20p11.21
18 238604_at		3.10	5.61E-12	3.10E-08	1.46	9.56	
19 209365_s_at	ECM1	3.14	3.60E-11	9.96E-08	1.49	9.52	1q21
20 201596_x_at	KRT18	7.58	2.11E-10	2.50E-07	1.56	9.52	12q13
21 202670_at	MAP2K1	3.60	5.03E-10	4.58E-07	1.59	9.45	15q22.1-q22.33
22 203320_at	LNK	3.09	1.34E-10	1.94E-07	1.50	9.37	12q24
23 210314_x_at	TNFSF13	4.88	2.77E-10	3.06E-07	1.53	9.36	17p13.1
24 209500_x_at	TNFSF13	4.05	4.42E-10	4.19E-07	1.55	9.34	17p13.1
25 221841_s_at		4.04	3.60E-11	9.96E-08	1.42	9.21	
26 235359_at		2.91	1.88E-10	2.49E-07	1.47	9.20	
27 223249_at	CLDN12	3.53	1.06E-10	1.77E-07	1.44	9.16	7q21
28 218217_at	RISC	3.35	1.12E-10	1.77E-07	1.43	9.10	17q23.1
29 201739_at	SGK	4.42	4.17E-11	1.01E-07	1.40	9.07	6q23

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
30	229309_at		11.50	3.64E-09	1.89E-06	1.64	9.01	
31	240572_s_at		3.26	9.26E-11	1.77E-07	1.39	8.95	
32	208683_at	CAPN2	3.21	9.71E-11	1.77E-07	1.38	8.92	1q41-q42
33	225602_at	C9orf19	2.86	5.10E-11	1.13E-07	1.36	8.90	9p13-p12
34	226818_at	LOC219972	11.01	2.61E-09	1.63E-06	1.54	8.89	11q12.1
35	220974_x_at	BA108L7.2	4.78	3.85E-10	3.87E-07	1.39	8.79	10q24.31
36	229383_at		5.01	3.55E-09	1.87E-06	1.52	8.77	
37	212459_x_at	SUCLG2	3.54	8.98E-11	1.77E-07	1.34	8.72	3p14.2
38	205859_at	LY86	3.60	1.34E-09	1.01E-06	1.43	8.71	6p24.3
39	211084_x_at	PRKCN	4.82	2.26E-10	2.58E-07	1.33	8.60	2p21
40	236738_at		6.52	1.66E-09	1.20E-06	1.40	8.60	
41	217849_s_at	CDC42BPB	4.85	2.02E-10	2.50E-07	1.32	8.59	14q32.3
42	205330_at	MN1	9.06	1.06E-08	4.35E-06	1.56	8.52	22q12.1
43	204057_at	ICSBP1	4.27	5.50E-09	2.68E-06	1.44	8.46	16q24.1
44	228415_at	AP1S2	2.82	2.29E-09	1.52E-06	1.33	8.30	Xp22.31
45	202283_at	SERPINF1	8.45	2.79E-09	1.65E-06	1.34	8.29	17p13.1
46	226841_at	LOC219972	12.54	1.86E-08	6.29E-06	1.51	8.26	11q12.1
47	226137_at		3.27	4.82E-09	2.42E-06	1.36	8.26	
48	208033_s_at	ATBF1	3.76	1.34E-09	1.01E-06	1.30	8.24	16q22.3-q23.1
49	233555_s_at	SULF2	17.48	2.64E-08	8.12E-06	1.58	8.19	20q12-13.2
50	205076_s_at	CRA	5.49	1.56E-08	5.96E-06	1.44	8.19	1q12-q21

4.8   inv(3) versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	212953_x_at	CALR	-5.95	2.17E-14	5.07E-11	-3.69	-18.88	19p13.3-p13.2
2	205382_s_at	DF	-12.24	2.37E-15	7.12E-12	-3.43	-18.68	19p13.3
3	203948_s_at	MPO	-9.29	4.98E-19	1.05E-14	-3.14	-18.57	17q23.1
4	203949_at	MPO	-6.22	1.52E-17	1.60E-13	-3.05	-17.82	17q23.1
5	200654_at	P4HB	-3.78	4.67E-17	3.27E-13	-2.71	-16.03	17q25
6	214450_at	CTSW	-8.62	1.58E-13	2.89E-10	-2.90	-15.67	11q13.1
7	231736_x_at	MGST1	-6.90	6.57E-16	2.30E-12	-2.57	-15.09	12p12.3-p12.1
8	224918_x_at	MGST1	-6.02	2.58E-16	1.15E-12	-2.54	-15.02	12p12.3-p12.1
9	206871_at	ELA2	-6.28	2.73E-16	1.15E-12	-2.54	-15.00	19p13.3
10	214575_s_at	AZU1	-12.19	2.49E-13	3.73E-10	-2.58	-14.34	19p13.3
11	205624_at	CPA3	-21.54	5.79E-12	5.79E-09	-2.85	-14.33	3q21-q25
12	208689_s_at	RPN2	-2.77	3.65E-15	9.58E-12	-2.43	-14.27	20q12-q13.1
13	238022_at		-8.14	1.08E-12	1.33E-09	-2.28	-12.89	
14	38487_at	STAB1	-5.21	5.94E-13	8.31E-10	-2.23	-12.76	3p21.31
15	221004_s_at	ITM2C	-4.36	8.93E-14	1.88E-10	-2.12	-12.49	2q37
16	217716_s_at	SEC61A1	-2.51	1.65E-13	2.89E-10	-2.09	-12.25	3q21.3
17	221739_at	IL27w	-2.24	2.31E-13	3.73E-10	-2.06	-12.11	19p13.3
18	233072_at	KIAA1857	-10.04	1.05E-10	5.14E-08	-2.37	-12.06	9q34
19	208852_s_at	CANX	-2.94	3.24E-12	3.78E-09	-2.07	-11.86	5q35

20	220798_x_at	FLJ11535	-5.26	7.78E-12	6.81E-09	-2.05	-11.62	19p13.3
21	217225_x_at	LOC283820	-2.41	9.52E-13	1.25E-09	-1.94	-11.43	16p13.13
22	208730_x_at	RAB2	2.53	8.63E-10	3.12E-07	2.18	11.42	8q12.1
23	203675_at	NUCB2	-3.92	6.96E-12	6.65E-09	-2.00	-11.42	11p15.1-p14
24	201004_at	SSR4	-2.77	1.64E-11	1.15E-08	-2.00	-11.33	Xq28
25	210788_s_at	retSDR4	-2.65	7.69E-12	6.81E-09	-1.95	-11.22	14q22.3
26	202759_s_at	AKAP2	-4.78	2.58E-11	1.69E-08	-1.98	-11.15	9q31-q33
27	209619_at	CD74	4.57	1.47E-11	1.14E-08	1.92	11.07	5q32
28	214315_x_at	CALR	-3.14	2.25E-11	1.52E-08	-1.93	-11.00	19p13.3-p13.2
29	229168_at	DKFZp434K0621	-5.62	4.18E-10	1.72E-07	-2.12	-10.99	5q35.3
30	211990_at	HLA-DPA1	12.02	1.70E-08	3.31E-06	2.38	10.92	6p21.3
31	214797_s_at	PCTK3	6.22	2.95E-09	8.48E-07	2.12	10.91	1q31-q32
32	211709_s_at	SCGF	-5.08	3.77E-12	3.96E-09	-1.80	-10.65	19q13.3
33	200068_s_at - HG-U133A	CANX	-1.76	3.59E-12	3.96E-09	-1.79	-10.61	5q35
34	206914_at	CRTAM	6.82	3.01E-09	8.54E-07	1.99	10.50	11q22-q23
35	204897_at	PTGER4	5.48	3.25E-10	1.37E-07	1.87	10.44	5p13.1
36	221253_s_at	MGC3178	-3.45	5.95E-11	3.62E-08	-1.81	-10.36	6p24.3
37	225010_at	D10S170	2.56	2.69E-11	1.71E-08	1.77	10.33	10q21
38	210140_at	CST7	-8.79	1.17E-09	4.09E-07	-1.98	-10.32	20p11.21
39	226905_at		-1.96	8.40E-11	4.20E-08	-1.78	-10.24	
40	200652_at	SSR2	-1.91	1.02E-11	8.61E-09	-1.73	-10.22	1q21-q23
41	33323_r_at	SFN	1.93	1.07E-11	8.68E-09	1.73	10.21	1p35.3
42	227353_at	EVER2	5.28	1.34E-08	2.75E-06	2.02	10.17	17q25.3
43	224839_s_at	GPT2	-6.13	8.34E-11	4.20E-08	-1.77	-10.15	16q12.1
44	200068_s_at - HG-U133B	CANX	-1.67	1.62E-11	1.15E-08	-1.72	-10.14	5q35
45	209215_at	TETRAN	-3.38	1.52E-11	1.14E-08	-1.72	-10.14	4p16.3
46	205614_x_at	MST1	-8.62	3.49E-09	9.53E-07	-2.00	-9.99	3p21
47	241383_at		-4.56	2.13E-09	6.47E-07	-1.87	-9.85	
48	214317_x_at	RPS9	2.30	1.38E-09	4.55E-07	1.77	9.82	19q13.4
49	202487_s_at	H2AV	-2.25	6.02E-11	3.62E-08	-1.64	-9.66	7p13
50	204661_at	CDW52	22.88	1.06E-07	1.35E-05	2.16	9.63	1p36

4.9   inv(3) versus t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-5.73	1.58E-13	3.73E-09	-2.14	-12.41	17q23.1
2	211084_x_at	PRKCN	6.08	3.25E-10	1.92E-06	1.92	10.59	2p21
3	225010_at	D10S170	2.96	1.16E-11	1.38E-07	1.78	10.37	10q21
4	233955_x_at	HSPC195	5.19	3.37E-08	8.86E-05	2.18	10.19	5q31.3
5	203948_s_at	MPO	-6.82	1.36E-10	1.07E-06	-1.74	-9.93	17q23.1
6	217963_s_at	NGFRAP1	29.01	4.74E-07	3.74E-04	2.04	8.67	Xq22.1
7	224516_s_at	HSPC195	5.87	5.57E-07	3.79E-04	1.92	8.45	5q31.3
8	219478_at	WFDC1	-12.35	6.15E-08	1.28E-04	-1.68	-8.45	16q24.3
9	217226_s_at	BA108L7.2	3.53	7.38E-08	1.28E-04	1.58	8.38	10q24.31
10	231180_at		-2.35	2.92E-09	1.38E-05	-1.42	-8.23	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
11	201281_at	ADRM1	-2.17	1.21E-08	4.62E-05	-1.45	-8.15	20q13.33
12	212423_at	FLJ90798	4.18	7.41E-08	1.28E-04	1.49	8.07	10q22.3
13	222996_s_at	HSPC195	4.31	1.08E-06	4.79E-04	1.79	7.98	5q31.3
14	228827_at		-95.46	2.85E-07	2.93E-04	-1.78	-7.91	
15	230259_at	.	-1.91	2.21E-08	6.52E-05	-1.37	-7.77	
16	213716_s_at	SECTM1	5.01	2.54E-07	2.86E-04	1.44	7.68	17q25
17	211709_s_at	SCGF	-3.55	1.37E-08	4.62E-05	-1.30	-7.56	19q13.3
18	202759_s_at	AKAP2	-4.91	2.29E-07	2.71E-04	-1.45	-7.56	9q31-q33
19	219165_at	PDLIM2	3.79	6.33E-07	4.00E-04	1.48	7.55	8p21.2
20	206478_at	KIAA0125	23.32	2.67E-06	8.31E-04	1.89	7.54	14q32.33
21	205529_s_at	CBFA2T1	-13.48	6.51E-07	4.00E-04	-1.63	-7.44	8q22
22	212895_s_at	ABR	3.03	3.97E-07	3.50E-04	1.38	7.38	17p13.3
23	223534_s_at	RPS6KL1	-2.20	8.42E-08	1.33E-04	-1.31	-7.37	14q24.2
24	212953_x_at	CALR	-2.47	3.99E-07	3.50E-04	-1.42	-7.33	19p13.3-p13.2
25	206295_at	IL18	3.69	1.85E-06	6.95E-04	1.52	7.33	11q22.2-q22.3
26	202006_at	PTPN12	2.76	6.85E-07	4.00E-04	1.39	7.29	7q11.23
27	220974_x_at	BA108L7.2	4.34	5.65E-07	3.79E-04	1.37	7.27	10q24.31
28	201243_s_at	ATP1B1	5.21	2.00E-06	7.03E-04	1.50	7.27	1q22-q25
29	201938_at	CDK2AP1	2.10	7.57E-08	1.28E-04	1.27	7.26	12q24.31
30	207839_s_at	LOC51754	3.16	2.14E-07	2.66E-04	1.30	7.24	9p13.1
31	203820_s_at	KOC1	3.93	2.73E-06	8.37E-04	1.53	7.19	7p11
32	202887_s_at	RTP801	4.32	1.72E-06	6.79E-04	1.44	7.17	10pter-q26.12
33	215051_x_at	AIF1	2.69	1.90E-07	2.49E-04	1.28	7.17	6p21.3
34	214042_s_at	RPL22	1.48	7.74E-07	4.16E-04	1.35	7.15	1p36.3-p36.2
35	227620_at		3.79	3.71E-07	3.50E-04	1.27	7.03	
36	210150_s_at	LAMA5	-4.17	5.29E-07	3.79E-04	-1.31	-7.01	20q13.2-q13.3
37	230659_at	KIAA0212	-2.09	5.37E-07	3.79E-04	-1.30	-6.99	3p26.1
38	221773_at		3.81	8.38E-07	4.31E-04	1.30	6.99	
39	226865_at		8.49	5.84E-06	1.21E-03	1.64	6.98	
40	242621_at	FLJ32468	-1.58	2.69E-07	2.90E-04	-1.24	-6.95	7q22.1
41	229406_at		-11.72	1.19E-06	4.98E-04	-1.39	-6.94	
42	214317_x_at	RPS9	2.15	7.51E-08	1.28E-04	1.19	6.93	19q13.4
43	213908_at		3.96	2.61E-06	8.24E-04	1.38	6.92	
44	204494_s_at	DKFZP434H132	4.90	6.20E-06	1.21E-03	1.56	6.89	15q22.33
45	214807_at		2.91	2.89E-06	8.66E-04	1.34	6.80	
46	220377_at	C14orf110	239.90	8.80E-06	1.40E-03	1.75	6.79	14q32.33
47	221458_at	HTR1F	2.55	2.14E-06	7.23E-04	1.30	6.77	3p12
48	227279_at	MGC15737	3.22	4.36E-06	1.08E-03	1.38	6.76	Xq22.1
49	206871_at	ELA2	-5.10	6.92E-07	4.00E-04	-1.22	-6.69	19p13.3
50	235199_at		2.76	1.11E-06	4.79E-04	1.22	6.68	

4.10 t(15;17) versus t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location

1	214450_at	CTSW	28.73	1.65E-13	4.59E-09	3.58	17.73 11q13.1
2	38487_at	STAB1	19.69	4.77E-13	4.59E-09	3.26	16.49 3p21.31
3	209732_at	CLECSF2	-30.76	2.95E-12	1.46E-08	-3.39	-16.10 12p13-p12
4	211990_at	HLA-DPA1	-10.92	1.76E-11	5.09E-08	-2.53	-13.40 6p21.3
5	224839_s_at	GPT2	12.98	6.62E-11	1.19E-07	2.37	12.32 16q12.1
6	212509_s_at		10.31	9.35E-11	1.59E-07	2.37	12.20
7	204150_at	STAB1	21.33	3.55E-10	4.10E-07	2.36	11.58 3p21.31
8	201596_x_at	KRT18	20.06	3.29E-10	3.96E-07	2.28	11.50 12q13
9	221004_s_at	ITM2C	3.37	4.65E-13	4.59E-09	1.86	11.42 2q37
10	205349_at	GNA15	3.53	3.47E-11	8.35E-08	2.00	11.42 19p13.3
11	205663_at	PCBP3	4.49	9.95E-12	3.59E-08	1.92	11.33 21q22.3
12	226878_at		-5.52	8.96E-10	7.61E-07	-2.06	-10.80
13	212953_x_at	CALR	2.41	1.19E-12	8.57E-09	1.74	10.78 19p13.3-p13.2
14	227326_at		5.43	2.89E-10	3.63E-07	1.89	10.58
15	217716_s_at	SEC61A1	2.09	3.73E-12	1.54E-08	1.70	10.48 3q21.3
16	228113_at	STAT3	-5.12	5.53E-10	5.50E-07	-1.86	-10.38 17q21
17	200986_at	SERPING1	9.81	1.47E-09	1.09E-06	1.98	10.34 11q12-q13.1
18	208689_s_at	RPN2	1.79	3.03E-12	1.46E-08	1.63	10.17 20q12-q13.1
19	217478_s_at	HLA-DMA	-5.35	6.89E-10	6.42E-07	-1.81	-10.15 6p21.3
20	204316_at	RGS10	-2.45	1.99E-10	2.67E-07	-1.73	-10.10 10q25
21	209021_x_at	KIAA0652	4.43	3.36E-11	8.35E-08	1.61	9.83 11p11.12
22	205614_x_at	MST1	7.54	3.75E-09	2.30E-06	1.83	9.69 3p21
23	209619_at	CD74	-4.60	1.28E-10	1.95E-07	-1.60	-9.66 5q32
24	200953_s_at	CCND2	2.70	4.02E-10	4.30E-07	1.65	9.66 12p13
25	208852_s_at	CANX	2.32	6.39E-11	1.19E-07	1.57	9.60 5q35
26	208826_x_at	HINT1	1.43	5.89E-11	1.19E-07	1.56	9.58 5q31.2
27	201522_x_at	SNRPN	-3.65	1.70E-11	5.09E-08	-1.53	-9.54 15q12
28	201136_at	PLP2	2.76	2.03E-10	2.67E-07	1.56	9.41 Xp11.23
29	201137_s_at	HLA-DPB1	-13.39	1.86E-08	7.79E-06	-1.93	-9.37 6p21.3
30	201425_at	ALDH2	5.16	1.10E-09	8.76E-07	1.61	9.35 12q24.2
31	204670_x_at	HLA-DRB5	-5.72	8.74E-10	7.61E-07	-1.58	-9.30 6p21.3
32	201952_at	ALCAM	4.64	2.50E-09	1.76E-06	1.65	9.30 3q13.1
33	211991_s_at	HLA-DPA1	-17.00	2.54E-08	9.11E-06	-1.85	-9.13 6p21.3
34	209312_x_at	HLA-DRB1	-6.80	5.84E-09	3.18E-06	-1.63	-9.09 6p21.3
35	238022_at		4.06	6.47E-11	1.19E-07	1.46	9.09
36	211474_s_at	SERPINB6	-5.69	1.90E-08	7.82E-06	-1.74	-9.06 6p25
37	223321_s_at	FGFRL1	3.74	4.94E-09	2.89E-06	1.61	9.02 4p16
38	201894_s_at	DCN	2.05	1.13E-10	1.81E-07	1.42	8.86 12q13.2
39	208885_at	LCP1	2.18	1.50E-10	2.16E-07	1.42	8.85 13q14.3
40	201923_at	PRDX4	-5.83	1.40E-08	6.42E-06	-1.61	-8.82 Xp22.13
41	209344_at	TPM4	6.87	2.27E-08	8.69E-06	1.69	8.80 19p13.1
42	227353_at	EVER2	-3.83	4.90E-09	2.89E-06	-1.52	-8.79 17q25.3
43	202732_at	PKIG	2.65	2.70E-09	1.79E-06	1.49	8.74 20q12-q13.1
44	208306_x_at	HLA-DRB4	-7.05	1.62E-08	7.08E-06	-1.57	-8.69 6p21.3
45	55093_at	CSGlcA-T	1.87	6.61E-10	6.36E-07	1.41	8.65 7q36.1
46	201360_at	CST3	4.20	2.73E-09	1.79E-06	1.45	8.61 20p11.21
47	221799_at	CSGlcA-T	2.51	3.90E-10	4.30E-07	1.38	8.59 7q36.1

48 201581_at	DJ971N18.2	2.54	2.69E-09	1.79E-06	1.44	8.58 20p12
49 207721_x_at	HINT1	1.55	5.39E-10	5.50E-07	1.38	8.52 5q31.2
50 205035_at	CTDP1	2.57	1.34E-08	6.42E-06	1.51	8.51 18q23